



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 143132

TO: Janet Epps-Ford  
Location: rem/2c05/2c18  
Art Unit: 1635  
Wednesday, July 13, 2005

Case Serial Number: 09/753169

From: Mary Jane Ruhl  
Location: Biotech-Chem Library  
Remsen 1-A-62  
Phone: 571-272-2524

[maryjane.ruhl@uspto.gov](mailto:maryjane.ruhl@uspto.gov)

### Search Notes

Examiner Epps-Ford,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524



THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-1  
Perfect score: 20  
Sequence: 1 ctaacacagtcattgtcca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Az46971 Bcl-Xl MR
2	20	100.0	559	12	Ach73889 Human gen
c 3	20	100.0	737	2	Aa81699 Human thy
c 4	20	100.0	737	10	Abz83507 Toxycolog
c 5	20	100.0	737	11	Adi32132 Human cdn
c 6	20	100.0	863	12	Adh52632 Chinese h
c 7	20	100.0	926	2	Aa81698 Human thy
c 8	20	100.0	926	2	Aat40079 Bcl-XL ge
c 9	20	100.0	926	3	Aaz93614 Bcl-x gen
c 10	20	100.0	926	4	Aas15189 Human bcl
c 11	20	100.0	926	4	Aac90810 Human bcl
c 12	20	100.0	926	6	Ak84766 Human cdn
c 13	20	100.0	926	8	Abt16641 Human bcl
c 14	20	100.0	926	10	Ad56779 Human bcl
c 15	20	100.0	926	10	Aad64187 Human bcl
c 16	20	100.0	926	11	Adi32104 Human cdn
c 17	20	100.0	926	12	Adh52630 Human ant
c 18	20	100.0	926	12	Adoi9990 Human PRO
c 19	20	100.0	926	12	Adp13351 Renal cel
c 20	20	100.0	1384	2	Aav17638 Mouse BCL
c 21	20	100.0	1466	10	Ade85177 Farnesyl

c 22	20	100.0	1742	4	Aaf75960 Rat wild-
c 23	20	100.0	1748	10	Adb58615 Toxigity-
c 24	20	100.0	1748	10	Adb53263 Primary r
c 25	20	100.0	2386	10	Adg89403 Cancer de
c 26	20	100.0	2386	12	Adn04260 Antipsori
c 27	20	100.0	2575	12	Adoi9865 Human PRO
c 28	18	90.0	21	6	Adv73037 Nucleotid
c 29	16.8	84.0	591	9	Adb10715 Alloioioc
c 30	16.8	84.0	591	9	Adb10717 Alloioioc
c 31	16.8	84.0	1509	6	Abk99834 Babesia c
c 32	16.8	84.0	1950	6	Abk99832 Babesia c
c 33	16.8	84.0	1959	6	Abk99865 Babesia c
c 34	16.8	84.0	2000	12	Adj41501 Plant cdn
c 35	16.8	84.0	2122	6	Abk99833 Babesia c
c 36	16.8	84.0	2157	6	Abk99831 Babesia c
c 37	16.8	84.0	2190	6	Abk99835 Babesia c
c 38	16.8	84.0	6509	6	Abk99835 Babesia c
c 39	16.8	84.0	110000	9	Abk99835 Babesia c
c 40	16.4	82.0	638	6	Abz15553 Arabidops
c 41	16.4	82.0	996	4	Aah71294 Human cer
c 42	16.4	82.0	2403	12	Adj40060 Plant cdn
c 43	16	80.0	20	3	Aaz93625 Antisense
c 44	16	80.0	20	5	Aah27670 Human bcl
c 45	16	80.0	20	10	Aad64198 Human bcl

ALIGNMENTS

RESULT 1  
AAZ46971  
ID AAZ46971 standard; DNA; 20 BP.  
XX  
AC AAZ46971;  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-Xl mRNA specific antisense oligo A.  
XX  
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Stein CA;  
XX  
DR WPI; 2000-137140/12.  
XX  
PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
XX  
PS Claim 1; Fig 1; 69pp; English.  
XX  
CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20

Db 1 CTCACACGATCCATTGTCCA 20

# RESULT 2

ACH73889

ID ACH73889 standard; DNA; 559 BP.

XX ACH73889;

AC ACH73889;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #7084.

DE Human; probe; ss; gene expression; single exon probe; microarray;

XX alternative splicing event; genomic alteration.

KW Homo sapiens.

OS US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 15; SEQ ID NO 7084; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 559;

Best Local Similarity 100.0%; Pred. No. 4.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20

Db 178 CTCACACGATCCATTGTCCA 197

# RESULT 3

AAQ81699/c

ID AAQ81699 standard; DNA; 737 BP.

XX AAQ81699;

AC AAQ81699;

DT 25-MAR-2003 (revised)

DT 10-AUG-1995 (first entry)

XX Human thymus BCL-XS DNA.

XX BCL-XS; apoptosis; cell death; cancer; neurodegenerative disease;

KW autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;

KW multiple sclerosis; ss.

XX Homo sapiens.

OS Key

Location/Qualifiers

CDS 135..647

/\*tag= a

XX WO9500642-A1.

XX 05-JAN-1995.

XX 22-JUN-1994; 94WO-US007089.

XX 22-JUN-1993; 93US-00081448.

XX (ARCH-) ARCH DEV CORP.

PA (UNMI ) UNIV MICHIGAN.

XX Thompson CB, Boise LH, Nunez G;

XX WPI; 1995-052079/07.

DR P-PSDB; AAR68888.

XX New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis -

PT and related vectors, recombinant cells and antibodies, useful in assay

PT and for control of cell death in e.g. neuronal cells, lymphocytes and

PT cancers.

XX Claim 5; Page 98; 127pp; English.

XX This DNA may be expressed recombinantly for the production of a BCL-X



CC protein, particularly with pcMV plasmids as vectors for expression in  
CC mammalian cell cultures. The protein has particular application in cancer  
CC cells (failure of programmed cell death (PCD)) or neurodegenerative and  
CC autoimmune diseases (premature PCD), e.g. Parkinson's disease,  
CC amyotrophic lateral sclerosis and multiple sclerosis. (Updated on 25-MAR  
CC -2003 to correct PN field.)

XX Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 737;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTCAACCAAGTCCATTGTCCA 20

Db 116 CTCAACCAAGTCCATTGTCCA 97

#### RESULT 4

ABZ83507/c

ID ABZ83507 standard; cDNA; 737 BP.

AC ABZ83507;

XX 14-MAY-2003 (first entry)

XX Toxicologically relevant human nucleotide sequence #666.

DE Toxicologically relevant gene; toxicological response; gene; ss.

XX Homo sapiens.

XX WO2003016500-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026514.

XX 16-AUG-2001; 2001US-0313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;

PI Alen P;

XX WPI; 2003-268322/26.

XX Claim 1; Page 226; 455pp; English.

XX The present invention describes a method (M1) for determining a  
CC toxicological response to an agent, which comprises comparing the  
CC expression profile of one or more human toxic response genes to a  
CC reference gene expression profile indicative of toxicity, and so  
CC determining the presence of a toxic response to the agent. Also  
CC described: (1) an array comprising one or more polynucleotides selected  
CC from the genes corresponding to the partial sequences given in ABZ82842  
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues  
CC ; and (2) determining if a gene putatively identified to be a toxic  
CC response gene plays a role on toxic response pathways by determining the  
CC expression profile of the gene after exposure of cells or a human subject  
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)  
CC exposing cells to an agent or isolating cells from a human subject who  
CC was exposed to an agent; (b) obtaining the test gene expression profile  
CC for a putatively identified toxic response gene after exposure to a known  
CC toxic pharmaceutical or industrial agent; and (c) comparing the test  
CC profile to the expression profile of a gene with a similar function or  
CC comparing the test profile to the expression profile of that gene after  
CC exposure to other known toxic compounds. The methods are useful for

CC predicting and determining toxicological responses on a cellular, organ  
CC or system level. The arrays comprising the human genes are useful for  
CC toxicological screening of drugs, pharmaceutical compounds and chemicals  
XX Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 737;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTCAACCAAGTCCATTGTCCA 20

Db 116 CTCAACCAAGTCCATTGTCCA 97

#### RESULT 5

ADI32132/c

ID ADI32132 standard; cDNA; 737 BP.

XX ADI32132;

XX 17-JUN-2004 (first entry)

XX Human cDNA #1458.

XX Human; gene; ss; immunological response; immunopathological condition;

XX Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;

XX irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;

XX acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;

XX osteopathic; antiarthritic; antirheumatic; cyostatic.

XX Homo sapiens.

XX US6607879-B1.

XX 19-AUG-2003.

XX 09-FEB-1998; 98US-00023655.

XX 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2003-895307/82.

XX A composition comprising a plurality of cDNAs, useful for detecting  
PT altered expression of genes in an immunological response or for  
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
PT or osteoarthritis.

XX Claim 1; SEQ ID NO 1458; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs  
CC for detecting the altered expression of genes in an immunological  
CC response. The invention also relates to a method of diagnosing or  
CC monitoring the treatment of an immunopathological condition in a sample,  
CC comprising obtaining nucleic acids from a sample, contacting the nucleic  
CC acids of the sample with an array comprising the plurality of cDNAs under  
CC conditions to form one or more hybridisation complexes, detecting the  
CC hybridisation complexes and comparing the levels of the detected  
CC hybridisation complexes with the level of hybridisation complexes  
CC detected in a non-diseased sample, where an altered level of the detected  
CC hybridisation complexes correlates with the presence of an  
CC immunopathological condition. Also disclosed are an expression profile  
CC comprising a microarray and a plurality of detectable complexes and a  
CC method for identifying a plurality of polynucleotide probes. The cDNAs  
CC are useful as hybridisable array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray can be used in  
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,  
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in

CC identifying agents for the treatment of the diseases. The microarray may  
CC also be used in drug discovery and development, toxicological and  
CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
CC genomic fragments. This sequence represents a human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification but was obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 11; Length 737;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACCAAGTCCATTGTCCA 20  
|||||  
Db 116 CTCACCAAGTCCATTGTCCA 97

## RESULT 6

ADH52632/c

ID ADH52632 standard; DNA; 863 BP.

XX

AC ADH52632;

XX

DT 25-MAR-2004 (first entry)

XX

DE Chinese hamster anti-apoptosis bcl-xL wild-type DNA.

XX

KW mammalian myeloma host cell; protein production; anti-apoptosis;

KW cell death; Chinese hamster; bcl-xL; wild-type; ds; gene.

XX

OS Crictulus griseus.

XX

PN US2003219871-A1.

XX

PD 27-NOV-2003.

XX

PF 28-MAR-2003; 2003US-00402017.

XX

PR 02-APR-2002; 2002US-0369307P.

XX

PA (BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.

XX

PI Enkel B, Meents H, Fussenegger M;

XX

DR WPI: 2004-033642/03.

XX

DR P-PSDB; ADH52633.

XX

PT New genetically engineered hamster or murine myeloma host cells  
comprising enhanced levels of active anti-apoptosis genes, useful for  
producing complex protein therapeutics.

XX

PS Claim 57; SEQ ID NO 3; 46pp; English.

XX

CC The invention relates to a novel mammalian host cell for producing  
CC protein therapeutics. The host cell comprises a hamster or a murine  
CC myeloma cell that is genetically modified by introduction of nucleic acid  
CC sequences encoding an anti-apoptosis gene, a selectable amplifiable  
CC marker gene and at least one gene of interest. The host cell of the  
CC invention may be useful for producing at least one protein encoded by a  
CC gene of interest. The DNA, polypeptide and the methods may be used for  
CC inhibiting or delaying cell death. The current sequence is that of the  
CC Chinese hamster anti-apoptosis bcl-xL wild-type DNA of the invention.

XX SQ Sequence 863 BP; 212 A; 227 C; 247 G; 177 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 863;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACCAAGTCCATTGTCCA 20

Db 51 CTCACCAAGTCCATTGTCCA 32  
|||||

## RESULT 7

AAQ81698/c

ID AAQ81698 standard; DNA; 926 BP.

XX

AC AAQ81698;

XX

DT 25-MAR-2003 (revised)

XX

DT 10-AUG-1995 (first entry)

XX

DE Human thymus BCL-XL DNA.

XX

KW BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;

KW autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;

KW multiple sclerosis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..836

FT /\*tag= a

XX

PN WO9500642-A1.

XX

PD 05-JAN-1995.

XX

PF 22-JUN-1994; 94WO-US007089.

XX

PR 22-JUN-1993; 93US-00081448.

XX

PA (ARCH-) ARCH DEV CORP.

PA (UNMI ) UNIV MICHIGAN.

XX

PI Thompson CB, Boise LH, Nunez G;

XX

DR WPI; 1995-052079/07.

XX

DR P-PSDB; AAR68887.

XX

PT New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis -  
and related vectors, recombinant cells and antibodies, useful in assay  
PT and for control of cell death in e.g. neuronal cells, lymphocytes and  
PT cancers.

XX

PS Claim 5; Page 94; 127pp; English.

XX

CC This DNA may be expressed recombinantly for the production of a BCL-X  
CC protein, particularly with pcmv plasmids as vectors for expression in  
CC mammalian cell cultures. The protein has particular application in cancer  
CC cells (failure of programmed cell death (PCD)) or neurodegenerative and  
CC autoimmune diseases (premature PCD), e.g. Parkinson's disease,  
CC amyotrophic lateral sclerosis and multiple sclerosis. (Updated on 25-MAR  
CC -2003 to correct PN field.)

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 926;

Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACCAAGTCCATTGTCCA 20

Db 116 CTCACCAAGTCCATTGTCCA 97

## RESULT 8

AAT40079/c

ID AAT40079 standard; cDNA; 926 BP.

XX

AC AAT40079;

XX



DE Human bcl-x cDNA.  
XX Human; antisense; IL-5R; bcl-x; ss; antiinfection; antiinflammatory;  
KW Cytostatic; inflammation; infection; tumour.  
XX Homo sapiens.  
OS WO200172765-A1.  
PN 04-OCT-2001.  
PD 28-MAR-2000; 2000WO-US008174.  
XX 28-MAR-2000; 2000WO-US008174.  
PR (ISIS-) ISIS PHARM INC.  
XX Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;  
PI Freier SM, McKay R, Karras JG;  
XX WPI; 2001-626250/72.  
DR Controlling cell behavior, useful e.g. for treatment of tumors, by  
PT modulating processing, e.g. splicing, of specific mRNA sequences with non  
PT -cleaving antisense agents.  
XX Example 15; Page 113; 121pp; English.  
PS The invention relates to controlling cell behaviour by modulating the  
XX processing of a selected wild-type mRNA target in the cell, is new. The  
CC mRNA is bound to a specific-binding antisense compound that does not  
CC cleave bound mRNA. The antisense oligonucleotides are useful as research  
CC reagents, diagnostic agents (in hybridisation assays), and for treatment  
CC or prevention of diseases, e.g. to prevent or delay infections,  
CC inflammation and tumours. The present sequence is the cDNA for the human  
XX bcl-x which is a target for antisense oligonucleotides if the invention  
XX  
SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 926;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCACCGAGTCCATTGTCCA 20  
Db 116 CTCACCGAGTCCATTGTCCA 97  
RESULT 11  
AAC90810/c  
ID AAC90810 standard; cDNA; 926 BP.  
XX AAC90810;  
AC 16-MAR-2001 (first entry)  
XX Human Bcl-xL nucleotide sequence SEQ ID NO:3.  
DE Human; Bcl-2; Bcl-xL; Bax; VDAC; apoptosis inhibitor; detection;  
XX apoptosis promoter; diagnosis; ss.  
KW Homo sapiens.  
OS JP2000287689-A.  
XX 17-OCT-2000.  
PD 08-APR-1999; 99JP-00101888.  
XX 08-APR-1999; 99JP-00101888.  
PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX

DR WPI; 2001-065575/08.  
DR P-PSDB; AAB50538.  
XX Screening of an apoptosis inhibitor or promoter which can be used as a  
PT drug and a diagnostic agent for various diseases caused by apoptosis  
PT inhibition or apoptosis promotion.  
XX Claim 16; Page 14-15; 22pp; Japanese.  
PS The present invention describes a method for screening for an apoptosis  
XX inhibitor or an apoptosis promoter in which VDAC-liposome, an index  
CC substance which can pass VDAC and a sample are incubated and the change  
CC in the concentration of the index substance during the incubation is  
CC detected to judge the presence of apoptosis inhibition or apoptosis  
CC promotion. The apoptosis inhibitor or the apoptosis promoter can be used  
CC as a drug and a diagnostic agent for various diseases caused by apoptosis  
CC inhibition or apoptosis promotion. The present sequence encodes the human  
CC Bcl-xL protein, which is an apoptosis inhibitor used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 926;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCACCGAGTCCATTGTCCA 20  
Db 116 CTCACCGAGTCCATTGTCCA 97  
RESULT 12  
ABK84766/c  
ID ABK84766 standard; cDNA; 926 BP.  
XX ABK84766;  
AC 14-AUG-2002 (first entry)  
XX Human cDNA differentially expressed in granulocytic cells #1337.  
DE Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX Homo sapiens.  
OS WO200228999-A2.  
XX 11-APR-2002.  
PD 03-OCT-2001; 2001WO-US030821.  
XX 03-OCT-2000; 2000US-0237189P.  
XX (GENE-) GENE LOGIC INC.  
PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX WPI; 2002-435328/46.  
XX Detecting granulocyte activation by detecting differential expression of  
PT genes associated with granulocyte activation, which serves as diagnostic  
PT markers that is useful for monitoring disease states and drug toxicity.  
XX Claim 1; SEQ ID NO 1337; 114pp; English.  
PS The invention relates to detecting (M1) granulocyte (GC) activation  
XX

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing the  
 CC expression level to an expression level in an unactivated GC, where  
 CC differential expression of Gs is indicative of GCA. Also included are  
 CC modulating (M2) GA by contacting GC with an agent that alters the  
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
 CC capable of modulating GCA or an inflammation (especially chronic) in a  
 CC tissue, an allergic response in a subject, exposure of a subject to a  
 CC pathogen or sterile inflammatory disease using the gene expression  
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a  
 CC tissue, an allergic response in a subject, exposure of a subject to a  
 CC pathogen or sterile inflammatory disease, by detecting the level of  
 CC expression in a sample of the tissue of gene(s) from Gs, where the level  
 CC of expression of the gene is indicative of inflammation; (4) treating  
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease, by contacting a tissue having inflammation with an  
 CC agent that modulates the expression of gene(s) from Gs in the tissue. M1  
 CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful  
 CC for screening an agent capable of modulating GCA preferably in an  
 CC inflammation in a tissue; M4 is useful for detecting an inflammation  
 CC (especially chronic) in a tissue, an allergic response in a subject,  
 CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.  
 CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,  
 CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult  
 CC respiratory distress syndrome, inflammatory bowel disease, Crohn's  
 CC disease, ulcerative colitis, periodontal disease; also bacterial  
 CC infection, viral infection, parasitic infection, protozoal infection,  
 CC fungal infection and M5 is useful for treating one of the above  
 CC conditions. The present sequence represents a gene differentially  
 CC expressed in granulocytes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACACGTCCTCATGTGCCA 20  
 |||||  
 Db 116 CTCACACGTCCTCATGTGCCA 97

#### RESULT 13

ID ABT16641/c  
 ID ABT16641 standard; DNA; 926 BP.

AC ABT16641;

DT 03-APR-2003 (first entry)

DE Human bcl-2 gene SEQ ID No 3.

KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;  
 KW radiation therapy; catalytic domain; enzyme; human; ds.

XX Homo sapiens.

XX WO200299090-A1.

XX 12-DEC-2002.

XX 07-JUN-2002; 2002WO-AU000739.

XX 07-JUN-2001; 2001AU-00005527.

XX (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.

XX Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;

XX

DR WPI; 2003-140617/13.

XX Novel DNazyme useful for treating tumors, and for enhancing the  
 PT sensitivity of malignant or virus infected cells to therapy, comprises a  
 PT catalytic domain and binding domain contiguous to the catalytic domain.

PS Disclosure; Page 44; 67pp; English.

XX The invention relates to a DNazyme which specifically cleaves mRNA  
 CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise  
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
 CC the catalytic domain, and therefore hybridise with, the two regions  
 CC immediately flanking the purine residue of the cleavage site within the  
 CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A  
 CC pharmaceutical composition comprising a DNazyme of the invention is  
 CC useful for treating tumors in a subject, and for enhancing the  
 CC sensitivity of malignant or virus infected cells to  
 CC therapy. The DNazymes are useful in diagnostics, therapeutics,  
 CC prophylaxis, research agents and in kits. The DNazymes are also useful  
 CC for increasing the susceptibility of tumour cells to anti-tumour  
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
 CC sequence represents a human bcl-2 gene of the invention

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCACACGTCCTCATGTGCCA 20  
 |||||  
 Db 116 CTCACACGTCCTCATGTGCCA 97

#### RESULT 14

ADD56779/c

ID ADD56779 standard; DNA; 926 BP.

XX

XX ADD56779;

DT 15-JAN-2004 (first entry)

XX Human bcl-xL nucleic acid sequence #SEQ ID 1.

XX Cytostatic; murine myeloma cell; anti-apoptosis gene;  
 KW biopharmaceutical protein; bcl-xL; apoptosis; ds.

XX Homo sapiens.

XX EP1348758-A1.

XX 01-OCT-2003.

XX 28-MAR-2002; 2002EP-00007144.

XX 28-MAR-2002; 2002EP-00007144.

XX (BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.

XX Ehenkel B, Meents H, Fussenegger M;

XX WPI; 2003-781115/74.

XX New genetically modified host cells comprising nucleic acid sequences  
 PT that encode for an anti-apoptosis gene, a selectable amplifiable marker  
 PT gene or at least one gene, useful for producing biopharmaceutical  
 PT proteins.

XX Claim 9; SEQ ID NO 1; 42pp; English.

XX The invention relates to a hamster host cell or a murine myeloma cell  
 CC genetically modified by introducing nucleic acid sequences that encode  
 CC for an anti-apoptosis gene, a selectable amplifiable marker gene or at

CC least one gene of interest. The cells are useful for the production of at  
CC least one protein encoded by a gene of interest, particularly for the  
CC production of biopharmaceutical proteins. The genetically engineered host  
CC cells have improved survival properties and enhanced level of active anti  
CC -apoptosis genes compared to non-transfected as well as non-amplified  
CC parental cells. The current sequence represents a bcl-xL nucleic acid  
CC sequence.

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 926;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCCAGTCCATTGTCCA 20  
|||  
Db 116 CTCAACCCAGTCCATTGTCCA 97

RESULT 15

AAD64187/c  
ID AAD64187 standard; DNA; 926 BP.

XX AC AAD64187;

DT 12-FEB-2004 (first entry)

XX DE Human bcl-x DNA.

XX KW Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;  
KW retinitis pigmentosa; myocardial infarction; neuroprotective; cytosstatic;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;  
KW neurotropic; anticonvulsant; vasotropic; therapy; cerebroprotective;  
KW stroke; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 135..836  
FT /tag= a  
FT /product= "Human bcl-x protein"

XX PN US2003191300-A1.

XX PD 09-OCT-2003.

XX PF 21-NOV-2002; 2002US-00302262.

XX PR 07-OCT-1998; 98US-00167921.

XX PR 26-MAR-1999; 99US-00277020.

XX PR 02-JUN-1999; 99US-00323743.

XX PR 12-DEC-2000; 2000US-00734846.

XX PA (BENN/) BENNETT C F.

XX PA (DEAN/) DEAN N M.

XX PA (MONI/) MONIA B P.

XX PA (NICK/) NICKOLOFF B J.

XX PA (ZHAN/) ZHANG Q Q.

XX PI Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;

XX DR WPI; 2003-864192/80.

XX DR P-PSDB; ABW02410.

XX PT Compound useful for treating reduced apoptotic conditions e.g. cancer

XX PT comprises nucleobases targeted to nucleic acid molecule encoding human

XX PT gene encoding intracellular membrane protein.

XX PS Claim 1; SEQ ID NO 1; Opp; English.

CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet  
CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention  
CC is useful for treating acquired immune deficiency syndrome (AIDS),  
CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy  
CC and ischaemia such as myocardial infarction and stroke. The present  
CC sequence is human bcl-x DNA

XX SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 926;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCCAGTCCATTGTCCA 20  
|||  
Db 116 CTCAACCCAGTCCATTGTCCA 97

Search completed: February 4, 2005, 21:52:35

Job time : 263.033 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169a-1  
Perfect score: 20  
Sequence: 1 ctcaaccagtcattgtcca 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235149
2	20	100.0	20	6	BD235162
3	20	100.0	20	6	BD235163
C 4	20	100.0	137	9	AY263337
C 5	20	100.0	328	9	AY263336
C 6	20	100.0	388	9	AY263335
C 7	20	100.0	512	6	CQ727769
C 8	20	100.0	737	6	AR054022
C 9	20	100.0	737	6	AR172595
C 10	20	100.0	737	6	IS2012
C 11	20	100.0	737	6	AR371662
C 12	20	100.0	737	6	AR380913
C 13	20	100.0	737	9	HSBCLXS
C 14	20	100.0	764	10	RNU10579
C 15	20	100.0	765	4	AF164517
C 16	20	100.0	863	6	AX925688
C 17	20	100.0	926	6	AR054021
C 18	20	100.0	926	6	AR118504
C 19	20	100.0	926	6	AR124952

C 20	20	100.0	926	6	AR144311
C 21	20	100.0	926	6	AR172594
C 22	20	100.0	926	6	BD243042
C 23	20	100.0	926	6	CQ765842
C 24	20	100.0	926	6	E58777
C 25	20	100.0	926	6	IS2011
C 26	20	100.0	926	6	AR371661
C 27	20	100.0	926	6	AR380885
C 28	20	100.0	926	6	AX839772
C 29	20	100.0	926	6	AX925686
C 30	20	100.0	926	9	HSBCLXL
C 31	20	100.0	979	10	MUSECLX
C 32	20	100.0	1011	9	HUMBCLXP
C 33	20	100.0	1235	10	MMU10102
C 34	20	100.0	1384	6	AR242207
C 35	20	100.0	1384	10	MMU51277
C 36	20	100.0	1466	6	AX775078
C 37	20	100.0	1466	10	MMU51278
C 38	20	100.0	1742	6	BD012974
C 39	20	100.0	1742	6	BD013799
C 40	20	100.0	1742	10	RNU72350
C 41	20	100.0	1748	6	AX827805
C 42	20	100.0	1748	10	RNU72349
C 43	20	100.0	1911	10	MMBCLAP1
C 44	20	100.0	2097	10	MMU51279
C 45	20	100.0	2375	10	AY141038

#### ALIGNMENTS

RESULT 1  
BD235149 20 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD235149 20 bp DNA linear PAT 17-JUL-2003  
Oligonucleotide inhibitors of bcl-xL.  
BD235149  
BD235149.1 GI:33044919  
JP 2002519048-A/1.  
synthetic construct  
synthetic construct  
artificial sequences.  
1 (bases 1 to 20)  
Stein, C.A.  
Oligonucleotide inhibitors of bcl-xL  
Patent: JP 2002519048-A 1 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
OS Artificial Sequence  
PN JP 2002519048-A/1  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC  
C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC  
A61K47/42,  
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCAACCAGTCATTGTCCA 20  
|||||

```
Db          1  CTCACACGATCCATTGTCCA 20

RESULT 2
LOCUS      BD235162
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235162
VERSION    BD235162.1 GI:33044932
KEYWORDS   JP 2002519048-A/14.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein, C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 14 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/14
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC

C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC
A61K47/42,
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
FH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT misc_binding (6)..(7)
FT misc_binding (10)..(12)
FT misc_binding (14)..(15)
FT misc_binding (17)..(20)
FT modified_base (1)..(1)
FT modified_base (2)..(2)
FT modified_base (3)..(3)
FT modified_base (6)..(6)
FT modified_base (7)..(7)
FT modified_base (10)..(10)
FT modified_base (11)..(12)
FT modified_base (14)..(15)
FT modified_base (17)..(17)
FT modified_base (18)..(19)

FEATURES             Location/Qualifiers
     source           1..20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  CTCACACGATCCATTGTCCA 20
    |||||
Db  1  CTCACACGATCCATTGTCCA 20

RESULT 4
LOCUS      AY263337/c
DEFINITION Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.
ACCESSION  AY263337
VERSION    AY263337.1 GI:30349284
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 137)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Yang, H., Sadda, M. and Lu, S.
JOURNAL    5'-alternative splicing of BCLX in HepG2
REFERENCE  2 (bases 1 to 137)
AUTHORS    Yang, H., Sadda, M. and Lu, S.

Db          1  CTCACACGATCCATTGTCCA 20

RESULT 3
LOCUS      BD235163
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235163
VERSION    BD235163.1 GI:33044933
KEYWORDS   JP 2002519048-A/15.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein, C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 15 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/15
```



TITLE Direct Submission  
 JOURNAL Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA  
 FEATURES  
 source 1. 137  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HepG2"  
 135. .>137  
 /note="BCLX; alternatively spliced"  
 /codon\_start=1  
 /product="BCL2L1"  
 /protein\_id="AAP22029.1"  
 /db\_xref="GI:30349285"  
 /translation="M"  
 CDS  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 9; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAACCAAGTCATTGTCCA 20  
 |||||  
 Db 116 CTCAACCAAGTCATTGTCCA 97  
 RESULT 5  
 AY263336/c  
 LOCUS Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.  
 DEFINITION  
 ACCESSION AY263336  
 VERSION AY263336.1 GI:30349282  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 328)  
 AUTHORS Yang H., Sada M. and Lu S.  
 TITLE 5'-alternative splicing of BCLX in HepG2  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 328)  
 AUTHORS Yang H., Sada M. and Lu S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA  
 FEATURES  
 source 1. 328  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HepG2"  
 326. .>328  
 /note="BCLX; alternatively spliced"  
 /codon\_start=1  
 /product="BCL2L1"  
 /protein\_id="AAP22028.1"  
 /db\_xref="GI:30349283"  
 /translation="M"  
 CDS  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 9; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAACCAAGTCATTGTCCA 20  
 |||||  
 Db 307 CTCAACCAAGTCATTGTCCA 288  
 RESULT 6  
 AY263335/c

LOCUS AY263335 388 bp mRNA linear PRI 03-MAY-2003  
 DEFINITION Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.  
 ACCESSION AY263335  
 VERSION AY263335.1 GI:30349280  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 388)  
 AUTHORS Yang H., Sada M. and Lu S.  
 TITLE 5'-alternative splicing of BCLX in HepG2  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 388)  
 AUTHORS Yang H., Sada M. and Lu S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA  
 FEATURES  
 source 1. 388  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HepG2"  
 386. .>388  
 /note="BCLX; alternatively spliced"  
 /codon\_start=1  
 /product="BCL2L1"  
 /protein\_id="AAP22027.1"  
 /db\_xref="GI:30349281"  
 /translation="M"  
 CDS  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 9; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAACCAAGTCATTGTCCA 20  
 |||||  
 Db 367 CTCAACCAAGTCATTGTCCA 348  
 RESULT 7  
 CQ727769/c  
 LOCUS Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.  
 DEFINITION Sequence 13703 from Patent WO02068579.  
 ACCESSION CQ727769  
 VERSION CQ727769.1 GI:42294740  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 AUTHORS Kits, such as nucleic acid arrays, comprising a majority of  
 TITLE humanexons or transcripts, for detecting expression and other uses  
 thereof  
 JOURNAL Patent: WO 02068579-A 13703 06-SEP-2002;  
 PE Corporation (NY) (US)  
 FEATURES  
 source 1. 512  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAACCAAGTCATTGTCCA 20  
 |||||

Db 116 CTCACACGATCCATTGTCCA 97

RESULT 8  
LOCUS AR054022/c 737 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 8 from patent US 5834309.  
ACCESSION AR054022  
VERSION AR054022.1 GI:5978884  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.  
TITLE Vertebrate apoptosis gene: compositions and methods  
JOURNAL Patent: US 5834309-A 8 10-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..737  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 737;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
|||||  
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 11  
LOCUS AR371662/c 737 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 7 from patent US 6395510.  
ACCESSION AR371662  
VERSION AR371662.1 GI:34608659  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.  
TITLE Vertebrate apoptosis gene: compositions and methods  
JOURNAL Patent: US 6395510-A 7 28-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 737;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
|||||  
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 12  
LOCUS AR380913/c 737 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1458 from patent US 6607879.  
ACCESSION AR380913  
VERSION AR380913.1 GI:40088547  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological  
response gene expression  
JOURNAL Patent: US 6607879-A 1458 19-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..737  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 737;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
|||||  
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 10  
LOCUS I52012/c 737 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 7 from patent US 5646008.  
ACCESSION I52012  
VERSION I52012.1 GI:2473213  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.

Db 116 CTCACACGATCCATTGTCCA 97

RESULT 9  
LOCUS AR172595/c 737 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 8 from patent US 6303331.  
ACCESSION AR172595  
VERSION AR172595.1 GI:17912086  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.  
TITLE Vertebrate apoptosis gene: compositions and methods  
JOURNAL Patent: US 6303331-A 8 16-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..737  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 737;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
|||||  
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 9  
LOCUS AR172595/c 737 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 8 from patent US 6303331.  
ACCESSION AR172595  
VERSION AR172595.1 GI:17912086  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.  
TITLE Vertebrate apoptosis gene: compositions and methods  
JOURNAL Patent: US 6303331-A 8 16-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..737  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 737;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
|||||  
Db 116 CTCACACGATCCATTGTCCA 97

RESULT 10  
LOCUS I52012/c 737 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 7 from patent US 5646008.  
ACCESSION I52012  
VERSION I52012.1 GI:2473213  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS Thompson,C.B., Boise,L.H. and Nunez,G.

Db 116 CTCACACGATCCATTGTCCA 97

```

Db      116 CTCACCAAGTCATTGTCCA 97

RESULT 13
HSBCLXS/c
LOCUS      HSBCLXS          737 bp      mRNA      linear      PRI 12-JAN-1995
DEFINITION H. sapiens bcl-xS mRNA.
ACCESSION  Z23116 L20122
VERSION    Z23116.1 GI:623236
KEYWORDS   bcl-xS gene.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 737)
            Thompson, C.B.
            Direct Submission
            Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
            Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
            60637, USA
REMARK     revised by [3] MAT
REFERENCE  2 (bases 1 to 737)
            Boise, L.H., Gonzalez-Garcia, M., Postema, C.E., Ding, L., Lindsten, T.,
            Turka, L.A., Mao, X., Nunez, G. and Thompson, C.B.
            bcl-x, a bcl-2-related gene that functions as a dominant regulator
            of apoptotic cell death
            Cell 74 (4), 597-608 (1993)
JOURNAL    93364977
MEDLINE    8358789
REFERENCE  3 (bases 1 to 737)
            Thompson, C.B.
            Direct Submission
            Submitted (12-JAN-1995) Craig B Thompson, Howard Hughes Medical
            Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
            60637, USA
COMMENT    On Jan 13, 1995 this sequence version replaced gi:510902.
FEATURES   Location/Qualifiers
            source          1..737
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="bcl-xS"
                        /cell_type="peripheral blood T cell"
                        /dev_stage="Adult"
                        135..647
            gene            /gene="bcl-xS"
            CDS             135..647
                        /gene="bcl-xS"
                        /codon_start=1
                        /protein_id="CAA80662.1"
                        /db_xref="GI:623237"
                        /db_xref="Swiss-Prot:Q07817"
                        /translation="MSOSNRELVDLSYKLSOKGYSWQSDVEENRTAPECTESE
                        NETSAINGNPWSHLADSPVNGATGHSSSLDAREVIPMAVKQALREAGDEFLRYR
                        RAFSDLTSLQHTPGTAYQSFQVWELFRDGVNWRIVAFVFFGGALCVESVQKEMQ
                        VLSRIASWMTATVLDHLEPWIQENGSGWDFVDLYGNNAAESRKQERFNRFILTMG
                        VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTCACCAAGTCATTGTCCA 20
        |||||
Db      20 CTCACCAAGTCATTGTCCA 1

RESULT 15
AF164517/c
LOCUS      AF164517          766 bp      mRNA      linear      MAM 01-AUG-2000
DEFINITION Ovis aries Bcl-x long protein mRNA, complete cds.
ACCESSION  AF164517
VERSION    AF164517.1 GI:9621785
KEYWORDS   Ovis aries (sheep)
SOURCE     Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Caprinae; Ovis.
REFERENCE  1 (bases 1 to 766)
            Murray, J.F., Dong, Y.B., Leigh, A.J., Scaramuzzi, R.J. and Carter, N.D.
            Bcl-x in the sheep ovary
            Unpublished
REFERENCE  2 (bases 1 to 766)
            Murray, J.F., Dong, Y.B., Leigh, A.J., Scaramuzzi, R.J. and Carter, N.D.
            Direct Submission
            Submitted (01-JUL-1999) Obstetrics and Gynaecology, St. George's
            Hospital Medical School, Cranmer Terrace, London SW17 0RE, UK
FEATURES   Location/Qualifiers
            source          1..766
                        /organism="Ovis aries"
                        /mol_type="mRNA"
                        /db_xref="taxon:9940"
                        /tissue_type="ovary"

KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 764)
            Wesselingh, S.L., David, G.L., Choi, S., Veluona, M. and Hardwick, J.M.
            Cloning and expression of rat bcl-x in cultured neurons
            Unpublished
REFERENCE  2 (bases 1 to 764)
            Hardwick, J.M.
            Direct Submission
            Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins
            School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681,
            USA
FEATURES   Location/Qualifiers
            source          1..764
                        /organism="Rattus norvegicus"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:10116"
                        /tissue_type="brain"
                        39..740
            gene            /gene="bcl-x"
            CDS             39..740
                        /gene="bcl-x"
                        /codon_start=1
                        /product="Bcl-x"
                        /protein_id="AAAL9257.1"
                        /db_xref="GI:505699"
                        /translation="MSQSNRELVDLSYKLSOKGYSWQSDVEENRTAPECTEPE
                        RETPSAINGNPWSHLADSPVNGATGHSSSLDAREVIPMAVKQALREAGDEFLRYR
                        RAFSDLTSLQHTPGTAYQSFQVWELFRDGVNWRIVAFVFFGGALCVESVQKEMQ
                        VLSRIASWMTATVLDHLEPWIQENGSGWDFVDLYGNNAAESRKQERFNRFILTMG
                        TVAGVLLGSLFSRK"

```

CDS  
41..742  
/note="anti-apoptotic Bcl-2 gene family member; Bcl-x  
short protein identified by PCR"  
/codon\_start=1  
/product="Bcl-x long protein"  
/protein\_id="AAF89532.1"  
/db\_xref="GI:9621786"  
/translation="MSQSNRELIVDFLSYKLSQKGYWSQFSDVDEENRTEAPEGTESD  
METPSAINGNSWHLADSPAVNGATGHSKSLDAREVIPMAAVKQALREAGDEFELRYR  
RAFSDLTSQLHITPGTAYQSFEQVNVNELFRDGVNMGRIIVAFFSGGALCVESVDKEMQ  
VLVSRITATWMTVLYNDHLEPWTIQENGWDTFVELYGNNAAESRKQERFNRWFLTGM  
TVAGVLLGSLFSRK"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 766;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCACCAAGTCATTCCTCA 20  
Db 22 CTCACCAAGTCATTCCTCA 3

Search completed: February 4, 2005, 23:30:32  
Job time : 485.738 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-1

Perfect score: 20

Sequence: 1 ctcaaccagtcattgtcca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gssi.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	136	9	CG608749
C 2	20	100.0	149	4	BG684338
C 3	20	100.0	151	2	BE386533
C 4	20	100.0	177	2	BF688810
C 5	20	100.0	198	2	BE407849
C 6	20	100.0	200	1	AA351198
C 7	20	100.0	210	4	BG334446
C 8	20	100.0	213	4	BG478819
C 9	20	100.0	218	4	BG752203
C 10	20	100.0	223	2	BE727284
C 11	20	100.0	225	2	BF026532
C 12	20	100.0	227	2	BE275637
C 13	20	100.0	228	4	BG489250
C 14	20	100.0	230	2	BF685843
C 15	20	100.0	232	4	BG746689
C 16	20	100.0	239	2	BE728507
C 17	20	100.0	248	2	BE386614
C 18	20	100.0	251	4	BM049633
C 19	20	100.0	252	2	BE560320
C 20	20	100.0	254	7	T28063
C 21	20	100.0	262	4	BG479739
C 22	20	100.0	275	4	BM012517
C 23	20	100.0	287	5	BY236510
C 24	20	100.0	297	2	BF128036

C 25	20	100.0	301	4	BG419161
C 26	20	100.0	320	5	BY220922
C 27	20	100.0	322	2	AW125200
C 28	20	100.0	323	5	BY329071
C 29	20	100.0	325	5	BY191347
C 30	20	100.0	326	5	BY181507
C 31	20	100.0	327	5	BY209882
C 32	20	100.0	336	5	BY219527
C 33	20	100.0	339	1	AA232598
C 34	20	100.0	341	5	BY176914
C 35	20	100.0	343	5	BY333899
C 36	20	100.0	344	2	BB869154
C 37	20	100.0	344	5	BY333250
C 38	20	100.0	348	5	BY010071
C 39	20	100.0	350	5	BY058101
C 40	20	100.0	353	5	BY016163
C 41	20	100.0	355	5	BY180189
C 42	20	100.0	355	5	BY212491
C 43	20	100.0	356	5	BY180646
C 44	20	100.0	356	6	CB813589
C 45	20	100.0	357	2	BB870590

ALIGNMENTS

RESULT 1  
CG608749/c  
LOCUS 136 bp DNA linear GSS 02-OCT-2003  
DEFINITION OST289185 Mus musculus 129Sv/Ev Mus musculus genomic clone  
OST289185, genomic survey sequence.  
ACCESSION CG608749  
VERSION CG608749.1 GI:37432598  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 136)  
AUTHORS Zambrowicz B.P., Abuin,A., Ramirez-Solis R., Richter, L.J.,  
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
COMMENT Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
FEATURES  
source  
1..136  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST289185"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 136;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCAACCAGTCATTGTCCA 20

```

Db      98  CTCACCAAGTCATTGTCCA 79
|||||
RESULT 2
BG684338/c
LOCUS      149 bp  mRNA  linear  EST 01-MAY-2001
DEFINITION 602636083F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763900 5',
mRNA sequence.
ACCESSION  BG684338
VERSION     BG684338.1  GI:13915735
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 149)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1620 row: e column: 21
           High quality sequence start: 6
           High quality sequence stop: 122.
           Location/Qualifiers
             1..149
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:4763900"
             /tissue_type="primary B-cells from tonsils (cell line)"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 48"
             /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
             Site 2: EcoRI; cDNA made by oligo-dT priming.
             Directionally cloned into EcoRI/XhoI sites using the
             following 5' adaptor: GGCACGAG(G). Size-selected >500bp
             for average insert size 1.8kb. Library constructed by Ling
             Hong in the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies).
             Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 100.0%; Score 20; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACCAAGTCATTGTCCA 20
|||||
Db 54 CTCACCAAGTCATTGTCCA 35
|||||

RESULT 3
BE386533/c
LOCUS      151 bp  mRNA  linear  EST 21-JUL-2000
DEFINITION 601273785F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614708 5',
mRNA sequence.
ACCESSION  BE386533
VERSION     BE386533.1  GI:9331898
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 151)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM156 row: n column: 24
           High quality sequence start: 2
           High quality sequence stop: 177.
           Location/Qualifiers
             1..177
             /organism="Homo sapiens"

```

```

REFERENCE  1  (bases 1 to 151)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC/DCTD/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM277 row: j column: 21
           High quality sequence stop: 151.
           Location/Qualifiers
             1..151
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:3614708"
             /tissue_type="melanotic melanoma"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 20"
             /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally
             cloned into EcoRI/XhoI sites using the following 5'
             adaptor: GGCACGAG(G). Size-selected >500bp for average
             insert size 1.8kb. Library constructed by Ling Hong in
             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies).".

FEATURES
source
Query Match 100.0%; Score 20; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACCAAGTCATTGTCCA 20
|||||
Db 85 CTCACCAAGTCATTGTCCA 66
|||||

RESULT 4
BF688810/c
LOCUS      177 bp  mRNA  linear  EST 22-DEC-2000
DEFINITION 602184955F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299479 5',
mRNA sequence.
ACCESSION  BF688810
VERSION     BF688810.1  GI:11974218
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 177)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM156 row: n column: 24
           High quality sequence start: 2
           High quality sequence stop: 177.
           Location/Qualifiers
             1..177
             /organism="Homo sapiens"

```

Query Match 100.0%; Score 20; DB 2; Length 198;  
Best Local Similarity 100.0%; Pred. No. 35;

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC/DCTP/DTP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI294 row: 1 column: 21  
 High quality sequence stop: 210.

**FEATURES**

source  
 1. .210  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4578596"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 20"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 Query Match 100.0%; Score 20; DB 4; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**ORIGIN**

Query Match 100.0%; Score 20; DB 4; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCACACGATCCATTGTCCA 20  
 ||||||||||||||||

DB 124 CTCACACGATCCATTGTCCA 105  
 ||||||||||||||||

**RESULT 8**

LOCUS BG478819/c 213 bp mRNA linear EST 21-MAR-2001  
 DEFINITION 60252369F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4643800 5', mRNA sequence.  
 ACCESSION BG478819 GI:13411098  
 VERSION BG478819  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 213)  
 NIH-MGC <http://mgc.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC/DCTP/DTP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI414 row: 1 column: 17  
 High quality sequence stop: 213.

**FEATURES**

source  
 1. .213  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /clone="IMAGE:4643800"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 20"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 Query Match 100.0%; Score 20; DB 4; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**ORIGIN**

QY 1 CTCACACGATCCATTGTCCA 20  
 ||||||||||||||||  
 DB 127 CTCACACGATCCATTGTCCA 108  
 ||||||||||||||||

**RESULT 9**

LOCUS BG752203/c 218 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602731335F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4874865 5', mRNA sequence.  
 ACCESSION BG752203  
 VERSION BG752203.1 GI:14062856  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 218)  
 NIH-MGC <http://mgc.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI755 row: e column: 10  
 High quality sequence stop: 218.  
 Location/Qualifiers  
 1. .218  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4874865"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 Note: this is a NIH\_MGC Library. |

**FEATURES**

source  
 1. .218  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4874865"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 Note: this is a NIH\_MGC Library. |

**ORIGIN**

Query Match 100.0%; Score 20; DB 4; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

Oy 1 CTCAACCAAGTCATTGTCCA 20
    |||||
Db 132 CTCAACCAAGTCATTGTCCA 113

RESULT 10
BE727284/c
LOCUS BE727284 223 bp mRNA linear EST 15-SEP-2000
DEFINITION 601560967F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830416 5',
mRNA sequence.
ACCESSION BE727284
VERSION BE727284.1 GI:10141377
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 223)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM504 row: f column: 17
High quality sequence start: 38
High quality sequence stop: 223.
Location/Qualifiers
FEATURES
    source
    1..223
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3830416"
    /tissue_type="melanotic melanoma"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_20"
    /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
    EcoRI; cDNA made by oligo-dT priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5',
    adaptor: GGCACGAG(G). Size-selected >500bp for average
    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match 100.0%; Score 20; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTCAACCAAGTCATTGTCCA 20
    |||||
Db 159 CTCACCAAGTCATTGTCCA 140

RESULT 12
BE275637/c
LOCUS BE275637 227 bp mRNA linear EST 13-JUL-2000
DEFINITION 601121162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988806 5',
mRNA sequence.
ACCESSION BE275637
VERSION BE275637.1 GI:9150595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 227)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM78 row: k column: 15
High quality sequence start: 27
High quality sequence stop: 227.
Location/Qualifiers
FEATURES
    source
    1..227
    /organism="Homo sapiens"
```

```

Oy 1 CTCAACCAAGTCATTGTCCA 20
    |||||
Db 157 CTCAACCAAGTCATTGTCCA 138

RESULT 11
BF026532/c
LOCUS BF026532 225 bp mRNA linear EST 10-OCT-2000
DEFINITION 601672487F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955413 5',
mRNA sequence.
ACCESSION BF026532
VERSION BF026532.1 GI:10734244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988806"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match          100.0%; Score 20; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCACTCCATTGTCCA 20
|||||
Db 161 CTCAACCACTCCATTGTCCA 142

RESULT 13
BG489250/c
LOCUS BG489250 228 bp mRNA linear EST 27-MAR-2001
DEFINITION mRNA sequence.
ACCESSION BG489250
VERSION BG489250
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMI396 row: k column: 16
High quality sequence stop: 228.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4636935"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/note="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match          100.0%; Score 20; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCACTCCATTGTCCA 20
|||||
Db 161 CTCAACCACTCCATTGTCCA 142

RESULT 13
BG489250/c
LOCUS BG489250 228 bp mRNA linear EST 27-MAR-2001
DEFINITION mRNA sequence.
ACCESSION BG489250
VERSION BG489250
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMI396 row: k column: 16
High quality sequence stop: 228.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4636935"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/note="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match          100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCACTCCATTGTCCA 20
|||||
Db 145 CTCAACCACTCCATTGTCCA 126

RESULT 14
BF685843/c
LOCUS BF685843 230 bp mRNA linear EST 22-DEC-2000
DEFINITION mRNA sequence.
ACCESSION BF685843
VERSION BF685843.1 GI:11971251
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 230)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMI169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4304288"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match          100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCACTCCATTGTCCA 20
|||||
Db 144 CTCAACCACTCCATTGTCCA 125

RESULT 15
BG746689/c
LOCUS BG746689 232 bp mRNA linear EST 15-MAY-2001
DEFINITION mRNA sequence.
ACCESSION BG746689
VERSION BG746689.1 GI:14057342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMI169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4304288"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match          100.0%; Score 20; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAACCACTCCATTGTCCA 20
|||||
Db 144 CTCAACCACTCCATTGTCCA 125

RESULT 15
BG746689/c
LOCUS BG746689 232 bp mRNA linear EST 15-MAY-2001
DEFINITION mRNA sequence.
ACCESSION BG746689
VERSION BG746689.1 GI:14057342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMI169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4304288"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 232)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: ATCC

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI709 row: d column: 04  
 High quality sequence stop: 232.

FEATURES  
 source

Location/Qualifiers  
 1. .232  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4857171"  
 /tissue\_type="adenocarcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_15"  
 /note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCACCGAGTCCATTGTCCA 20  
 Db 146 CTCACCGAGTCCATTGTCCA 127

Search completed: February 5, 2005, 08:11:23  
 Job time : 2391.67 secs

THIS PAGE LEFT BLANK

SUMMARIES				
Result No.	Score	Query		Description
		Match	Length	
1	20	100.0	20	6 AR124971 Sequence
2	20	100.0	20	6 AR144314 Sequence
3	20	100.0	20	6 BD235150 Oligonucle
4	20	100.0	20	6 BD235164 Oligonucle
5	20	100.0	20	6 BD235184 Oligonucle
6	20	100.0	20	6 BD243061 Antisense
7	20	100.0	24	6 CQ816672 Sequence
8	20	100.0	24	6 AX017820 Sequence
9	20	100.0	24	6 BD137331 Different
10	20	100.0	30	6 AR176180 Sequence
11	20	100.0	30	6 BD178062 Stress-re
12	20	100.0	30	6 E55260 Stress-toler
13	20	100.0	31	6 BD084109 Method of
14	20	100.0	31	6 BD102203 Method fo
15	20	100.0	37	6 AX925704 Sequence
16	20	100.0	39	6 AR118505 Sequence
17	20	100.0	512	6 CQ727769 Sequence
18	20	100.0	513	10 MMU10100 Mus musculus
19	20	100.0	513	10 AF136230 Rattus no

Monia, B.P., Freier, S.M., McKay, R. and Karras, J.G.  
Alteration of cellular behavior by antisense modulation of mRNA

TITLE  
JOURNAL  
PROCESSING  
FEATURES  
source

Patent: US 6210892-A 42 03-APR-2001;  
Location/Qualifiers  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||  
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 3

LOCUS BD235150 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235150  
VERSION BD235150.1 GI:33044920  
KEYWORDS JP 2002519048-A/2.  
SOURCE synthetic construct  
ORGANISM artificial construct

REFERENCE 1 (bases 1 to 20)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 2 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/2  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,  
A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc\_binding (1) . . (4)  
FT misc\_binding (7) . . (8)  
FT misc\_binding (10) . . (13)  
FT misc\_binding (17) . . (20).

FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||  
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 5

LOCUS BD235184/c 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235184  
VERSION BD235184.1 GI:33044954  
KEYWORDS JP 2002519048-A/36.  
SOURCE synthetic construct  
ORGANISM artificial construct

REFERENCE 1 (bases 1 to 20)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 36 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/36  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,  
A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc\_binding (1) . . (4)  
FT misc\_binding (7) . . (8)  
FT misc\_binding (10) . . (13)  
FT misc\_binding (17) . . (20).

FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||  
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 4

LOCUS BD235164 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235164  
VERSION BD235164.1 GI:33044934  
KEYWORDS JP 2002519048-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct

artificial sequences.  
1 (bases 1 to 20)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 16 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/16  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,  
A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc\_binding (1) . . (4)  
FT misc\_binding (7) . . (8)  
FT misc\_binding (10) . . (13)  
FT misc\_binding (17) . . (20).

FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||  
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 5

LOCUS BD235184/c 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235184  
VERSION BD235184.1 GI:33044954  
KEYWORDS JP 2002519048-A/36.  
SOURCE synthetic construct  
ORGANISM artificial construct

REFERENCE 1 (bases 1 to 20)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 36 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/36  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,  
A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc\_binding (1) . . (4)  
FT misc\_binding (7) . . (8)  
FT misc\_binding (10) . . (13)  
FT misc\_binding (17) . . (20).

FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||  
Db 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 4

LOCUS BD235164 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235164  
VERSION BD235164.1 GI:33044934  
KEYWORDS JP 2002519048-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct

```

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGTTGCTCTGAGACAT 20
    |||||
Db 20 TCCCGTTGCTCTGAGACAT 1

RESULT 6
LOCUS      BD243061          20 bp      DNA          linear          PAT 17-JUL-2003
DEFINITION Antisense modulation of bcl-x expression.
ACCESSION  BD243061
VERSION     BD243061.1 GI:33052831
KEYWORDS   JP 2002526093-A/20
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS   Bennett,F.C., Dean,N.M., Monia,B.P., Nickoloff,B.J. and Zhang,Q.
TITLE     Antisense modulation of bcl-x expression
JOURNAL   Patent: JP 2002526093-A 20 20-AUG-2002;
          ISIS PHARMACEUTICALS INC
COMMENT   OS Artificial Sequence
          PN JP 2002526093-A/20
          PD 20-AUG-2002
          PF 28-SEP-1999 JP 2000574543
          PR 07-OCT-1998 US 09/167921,26-MAR-1999 US 09/277020 PR
          P2 02-JUN-1999 US 09/323743
          PI FRANK C BENNETT,NICHOLAS M DEAN,BRETT P MONIA,BRIAN J PI
          NICKOLOFF,
          PI QINGQING ZHANG
          PC C12N15/09,A61K31/337,A61K31/711,A61K31/7115,A61K31/
          712,
          PC A61K31/7125,A61K33/24,A61K48/00,A61P35/00,A61P43/00,C07H21/04,
          PC C12N5/10//
          PC C12N5/10,C12R1:91,C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
          Synthetic
          FH Key
          FT source
          FT Location/Qualifiers
          /organism='Artificial Sequence'.
          1..20
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGTTGCTCTGAGACAT 20
    |||||
Db 1 TCCCGTTGCTCTGAGACAT 20

RESULT 7
LOCUS      CQ816672/c       24 bp      DNA          linear          PAT 03-JUN-2004
DEFINITION Sequence 13 from Patent WO2004040018.
ACCESSION  CQ816672
VERSION     CQ816672.1 GI:48144938
KEYWORDS
SOURCE     synthetic construct
ORGANISM   synthetic construct
          artificial sequences.

REFERENCE 1 (bases 1 to 24)
AUTHORS   Schweighoffer,F., Bracco,L. and Tocque,B.
TITLE     Differential screening
JOURNAL   Patent: JP 2002505887-A 12 26-FEB-2002;
          EXONHIT THERAPEUTICS SA
COMMENT   OS Artificial Sequence
          PN JP 2002505887-A/12
          PD 26-FEB-2002

Query Match      100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGTTGCTCTGAGACAT 20
    |||||
Db 20 TCCCGTTGCTCTGAGACAT 1

RESULT 8
LOCUS      AX017820/c       24 bp      DNA          linear          PAT 07-SEP-2000
DEFINITION Sequence 13 from Patent WO9946403.
ACCESSION  AX017820
VERSION     AX017820.1 GI:10042426
KEYWORDS
SOURCE     synthetic construct
ORGANISM   synthetic construct
          artificial sequences.

REFERENCE 1
AUTHORS   Bracco,L., Tocque,B. and Schweighoffer,F.
TITLE     Qualitative differential screening
JOURNAL   Patent: WO 9946403-A 13 16-SEP-1999;
          BRACCO LAURENT (FR); TOCQUE BRUNO (FR); EXONHIT THERAPEUTICS S A
          (FR); SCHWEIGHOFFER FABRIEN (FR)
          Location/Qualifiers
          1..24
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="OLIGO"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGTTGCTCTGAGACAT 20
    |||||
Db 20 TCCCGTTGCTCTGAGACAT 1

RESULT 9
LOCUS      BD137331/c       24 bp      DNA          linear          PAT 18-SEP-2002
DEFINITION Differential screening.
ACCESSION  BD137331
VERSION     BD137331.1 GI:23232276
KEYWORDS   JP 2002505887-A/12.
SOURCE     synthetic construct
ORGANISM   synthetic construct
          artificial sequences.

REFERENCE 1 (bases 1 to 24)
AUTHORS   Schweighoffer,F., Bracco,L. and Tocque,B.
TITLE     Differential screening
JOURNAL   Patent: JP 2002505887-A 12 26-FEB-2002;
          EXONHIT THERAPEUTICS SA
COMMENT   OS Artificial Sequence
          PN JP 2002505887-A/12
          PD 26-FEB-2002

```

```

PF 11-MAR-1999 JP 2000535770
PR 11-MAR-1998 FR 98/02997
PI FABIEN SCHWEIGHOFFER, LAURENT BRACCO, BRUNO TOCQUE PC
C12Q1/68, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12N15/09, C12N15/09,
PC C12N5/00, C12N15/00, C12N15/00
CC Description of Artificial Sequence: OLIGO
FH Key Location/Qualifiers
FT source 1..24
/organism='Artificial Sequence'.
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

RESULT 10
AR176180/c
LOCUS AR176180 30 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6310272.
ACCESSION AR176180
VERSION AR176180.1 GI:17917479
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuhashi, I. and Malik, K.A.
TITLE Stress resistant plant in which cell death suppressing gene is
introduced and method for producing the same
JOURNAL Patent: US 6310272-A 6 30-OCT-2001;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

RESULT 11
BD178062/c
LOCUS BD178062 30 bp DNA linear PAT 16-APR-2003
DEFINITION Stress-resistant plant having cell-death inhibitory gene
transferred thereto and method of constructing the same.
ACCESSION BD178062
VERSION BD178062.1 GI:30015326
KEYWORDS JP 2002300822-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuhashi, I. and Malik, K.A.
TITLE Stress-resistant plant having cell-death inhibitory gene
transferred thereto and method of constructing the same
JOURNAL Patent: JP 2002300822-A 6 15-OCT-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES

PF 11-MAR-1999 JP 2000535770
PR 11-MAR-1998 FR 98/02997
PI FABIEN SCHWEIGHOFFER, LAURENT BRACCO, BRUNO TOCQUE PC
C12Q1/68, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12N15/09, C12N15/09,
PC C12N5/00, C12N15/00, C12N15/00
CC Description of Artificial Sequence: OLIGO
FH Key Location/Qualifiers
FT source 1..24
/organism='Artificial Sequence'.
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

RESULT 10
AR176180/c
LOCUS AR176180 30 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6310272.
ACCESSION AR176180
VERSION AR176180.1 GI:17917479
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuhashi, I. and Malik, K.A.
TITLE Stress resistant plant in which cell death suppressing gene is
introduced and method for producing the same
JOURNAL Patent: US 6310272-A 6 30-OCT-2001;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

RESULT 11
BD178062/c
LOCUS BD178062 30 bp DNA linear PAT 16-APR-2003
DEFINITION Stress-resistant plant having cell-death inhibitory gene
transferred thereto and method of constructing the same.
ACCESSION BD178062
VERSION BD178062.1 GI:30015326
KEYWORDS JP 2002300822-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ohashi, Y., Mitsuhashi, I. and Malik, K.A.
TITLE Stress-resistant plant having cell-death inhibitory gene
transferred thereto and method of constructing the same
JOURNAL Patent: JP 2002300822-A 6 15-OCT-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES

OS Unidentified
PN JP 2002300822-A/6
PD 15-OCT-2002
PF 01-FEB-2002 JP 2002026196
PI YUKO OHASHI, ICHIRO MITSUHASHI, CAMAL A MALIK
PC A01H5/00, C12N15/09//C12N5/10, C12N15/00, C12N5/00 CC Topology:
Linear;
CC Stress-resistant plant having cell-death inhibitory gene CC
transferred
CC thereto and method of constructing the same FH Key
Location/Qualifiers
FT source 1..30
/organism='Unidentified'.
FEATURES
source
1..30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

RESULT 12
E55260/c
LOCUS E55260 30 bp DNA linear PAT 18-JUN-2001
DEFINITION Stress-tolerant plant having cell death inhibitory gene transferred
thereinto and method for constructing the same.
ACCESSION E55260
VERSION E55260.1 GI:13019329
KEYWORDS JP 2000023583-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Yuko, O., Ichiro, M. and Camal, A.M.
TITLE Stress-tolerant plant having cell death inhibitory gene transferred
thereinto and method for constructing the same
JOURNAL Patent: JP 2000023583-A 6 25-JAN-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT OS Artificial Sequence
PN JP 2000023583-A/6
PD 25-JAN-2000
PF 14-JUN-1999 JP 1999167565
PR YUKO OHASHI, ICHIRO MITSUHASHI, CAMAL A MARIKU
PC A01H5/00, A01H1/00, C07H21/04, C07K14/47, C12N5/10, C12N15/09// PC
(C12N5/10, C12R1.91), (C12N15/09, C12R1.91), C12N5/00, C12N15/00, PC
(C12N5/00, C12R1.91), (C12N15/00, C12R1.91)
CC
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.
FEATURES
source
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCGGTTGCTCTGAGACAT 20
|||||
DB 20 TCCCGGTTGCTCTGAGACAT 1
|||||

```



```
RESULT 13
BD084109/c
LOCUS      BD084109          31 bp    DNA        linear        PAT 27-AUG-2002
DEFINITION Method of detecting protein-protein interaction.
ACCESSION  BD084109
VERSION    BD084109.1  GI:22629719
KEYWORDS   JP 2001327296-A/8.
SOURCE     synthetic construct
ORGANISM   artificial construct
REFERENCE  1 (bases 1 to 31)
AUTHORS    Kato,S., Eguchi,C. and Nagata,N.
TITLE      Method of detecting protein-protein interaction
JOURNAL    Patent: JP 2001327296-A 8 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Artificial Sequence
            PN JP 2001327296-A/8
            PD 27-NOV-2001
            PF 24-AUG-2000 JP 2000254418
            PI SEISHI KATO,CHIKASHI EGUCHI,NAOKI NAGATA
            PC C12N15/09,C12Q1/02//C07K14/47,(C12N15/09,C12R1:91),(C12Q1/02,
            PC C12R1:91)
            PC C12N15/00,(C12N15/00,C12R1:91)
            CC Synthesized Oligonucleotide
            FH Key
            FT source
            FT Location/Qualifiers
            FT /organism='Artificial Sequence'.

FEATURES             source
    source            1..31
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

ORIGIN
Query Match          100.0%; Score 20; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
Db 30 TCCCGGTTGCTCTGAGACAT 11

RESULT 14
BD102203/c
LOCUS      BD102203          31 bp    DNA        linear        PAT 27-AUG-2002
DEFINITION Method for detecting protein-protein interaction.
ACCESSION  BD102203
VERSION    BD102203.1  GI:22647777
KEYWORDS   WO 0168885-A/8.
SOURCE     synthetic construct
ORGANISM   artificial construct
REFERENCE  1 (bases 1 to 31)
AUTHORS    Kato,S., Eguchi,C., Nagata,N. and Otake,M.
TITLE      Method for detecting protein-protein interaction
JOURNAL    Patent: WO 0168885-A 8 20-SEP-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP,SEISHI KATO,CHIKASHI EGUCHI,NAOKI
            NAGATA, MIYAKO OTAKE
COMMENT    OS Artificial Sequence
            PN WO 0168885-A/8
            PD 20-SEP-2001
            PF 13-MAR-2001 WO 2001JP001973
            PR 15-MAR-2000 JP 00P 073095,24-AUG-2000 JP 00P 254418 PI
            SEISHI KATO,CHIKASHI EGUCHI,NAOKI NAGATA,MIYAKO OTAKE PC
            C12N15/79,G01N33/68//C12P21/02,C07K19/00
            CC Synthesized Oligonucleotide
            FH Key
            FT source
            FT Location/Qualifiers
            FT /organism='Artificial Sequence'.

FEATURES             source
    source            1..31
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

ORIGIN
Query Match          100.0%; Score 20; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
Db 30 TCCCGGTTGCTCTGAGACAT 11

RESULT 15
AX925704/c
LOCUS      AX925704          37 bp    DNA        linear        PAT 19-DEC-2003
DEFINITION Sequence 19 from Patent WO03083093.
ACCESSION  AX925704
VERSION    AX925704.1  GI:40244376
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Enkel,B., Meents,H. and Fusseneegger,M.
TITLE      Host cells having improved cell survival properties and methods to
            generate such cells
JOURNAL    Patent: WO 03083093-A 19 09-OCT-2003;
            Boehringer Ingelheim Pharma GmbH & Co. KG (DE)
FEATURES             source
    source            1..37
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Oligonucleotide (Eco-Bcl for)"

ORIGIN
Query Match          100.0%; Score 20; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTTGCTCTGAGACAT 20
    |||||
Db 36 TCCCGGTTGCTCTGAGACAT 17

Search completed: February 4, 2005, 23:30:36
Job time : 484.738 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-2

Perfect score: 20

Sequence: 1 tcccggtgtctgagacat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001as:\*

5: Geneseq2001bs:\*

6: Geneseq2002as:\*

7: Geneseq2002bs:\*

8: Geneseq2003as:\*

9: Geneseq2003bs:\*

10: Geneseq2003ce:\*

11: Geneseq2003de:\*

12: Geneseq2004s:\*

-Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Aaz46972 Bcl-Xl MR
2	20	100.0	20	3	Aaz93633 Antisense
3	20	100.0	20	4	Aas15192 Human bcl
4	20	100.0	20	5	Aah27678 Human bcl
5	20	100.0	20	6	Abv73650 Human bcl
6	20	100.0	20	9	Ada24239 Human bcl
7	20	100.0	20	10	Aad64206 Human bcl
8	20	100.0	20	10	Aad64265 Human bcl
9	20	100.0	20	10	Aad64264 Human bcl
10	20	100.0	20	10	Aad64263 Human bcl
11	20	100.0	30	2	Aav57313 5' primer
12	20	100.0	31	5	Aah43465 cDNA clon
13	20	100.0	31	12	Adm45992 Primer 1
14	20	100.0	37	12	Adh52648 RT-PCR pr
15	20	100.0	39	2	Aat40080 Primer fo
16	20	100.0	540	12	Adh52634 Chinese h
17	20	100.0	559	12	ACH73889 Human gen
18	20	100.0	564	12	ACH7595 Human gen
19	20	100.0	600	4	Abaa60917 Human foe
20	20	100.0	600	4	Aai40812 Probe #94
21	20	100.0	600	4	ABA28894 Probe #73

22	20	100.0	600	4	AAK35096
23	20	100.0	600	4	AAK09207
24	20	100.0	600	4	ABs34848 Human liv
25	20	100.0	600	6	ABs09558 Human gen
26	20	100.0	600	12	Adh52636 Chinese h
27	20	100.0	660	12	Adh52638 Chinese h
28	20	100.0	660	12	Adh52640 Chinese h
29	20	100.0	702	5	Aah43464 cDNA clon
30	20	100.0	702	12	Adm45994 Human apo
31	20	100.0	737	2	AAQ81699 Human thy
32	20	100.0	737	10	ABz83507 Toxicolog
33	20	100.0	737	11	Adi32132 Human CDN
34	20	100.0	739	12	Adg65218 Human Bcl
35	20	100.0	747	4	AAF30926 Human Bcl
36	20	100.0	747	12	ADG65209 Human Bcl
37	20	100.0	863	12	ADH52632 Chinese h
38	20	100.0	926	2	AAQ81698 Human thy
39	20	100.0	926	2	AAT40079 Bcl-XL ge
40	20	100.0	926	3	Aaz93614 Bcl-x gen
41	20	100.0	926	4	AAS15189 Human bcl
42	20	100.0	926	4	AAC90810 Human bcl
43	20	100.0	926	6	ABK84766 Human CDN
44	20	100.0	926	8	ABT16641 Human bcl
45	20	100.0	926	10	ADD56779 Human bcl

ALIGNMENTS

RESULT 1  
AAZ46972  
ID AAZ46972 standard; DNA; 20 BP.  
XX AC AAZ46972;  
XX AC  
DT 14-APR-2000 (first entry)  
XX Bcl-Xl mRNA specific antisense oligo B.  
DE Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX Homo sapiens.  
OS  
XX WC200001393-A2.  
XX PD 13-JAN-2000.  
XX PF 02-JUL-1999; 99WO-US015250.  
XX PR 02-JUL-1998; 98US-00109614.  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX Stein CA;  
XX WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-X1 mRNA  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
 |||||  
 DB 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 2  
 AAZ93633  
 ID AAZ93633 standard; DNA; 20 BP.  
 XX  
 AC AAZ93633.  
 XX  
 DT 16-AUG-2000 (first entry)  
 XX  
 DE Antisense oligonucleotide directed against bcl-x gene.  
 XX  
 XX Bcl-x; bcl-xs; antisense; therapy; apoptosis; splice site;  
 KW cell signalling molecule; ultraviolet radiation; UV; cancer;  
 KW chemotherapy; cytokine; human; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200020432-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 XX 28-SEP-1999; 99WO-US022448.  
 XX  
 PR 07-OCT-1998; 98US-00167921.  
 PR 26-MAR-1999; 99US-00277020.  
 PR 02-JUN-1999; 99US-00323743.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang Q;  
 XX  
 DR WPI; 2000-303730/26.  
 XX  
 PT Antisense oligonucleotides targeted to, and capable of inhibiting the  
 PT expression of, bcl-x nucleic acids, useful for sensitizing cancer cells  
 PT to apoptotic agents.  
 XX  
 XX Claim 3; Page 106; 115pp; English.

XX Antisense inhibition of bcl-x and bcl-xs expression results in apoptosis.  
 CC Antisense oligonucleotides directed against bcl-x alter the ratio of bcl-  
 CC x isoforms expressed by a cell or tissue (i.e. increases or decreases the  
 CC ratio of bcl-x1 to bcl-xs expressed) by altering the splicing of the RNA  
 CC encoding bcl-x. The antisense oligonucleotide is specifically targeted to  
 CC a transcript comprising two splice sites which when contacted with the  
 CC transcript, reduces the relative frequency of splicing at the second  
 CC splice site so that the resulting ratio of RNA splice products is  
 CC altered. The use of antisense compounds sensitises cells to the effects  
 CC of apoptotic stimulants such as a cellular signaling molecule,  
 CC ultraviolet radiation, a cancer chemotherapeutic drug (e.g. VP-16,  
 CC cisplatin or taxol), ceramide (e.g. staurosporine) or a cytokine which  
 CC causes mitochondrial dysfunction (especially loss of mitochondrial  
 CC membrane function). The antisense oligonucleotides may have a therapeutic  
 CC role in the treatment of cancer  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCCGGTTGCTCTGAGACAT 20  
 |||||  
 DB 1 TCCCGGTTGCTCTGAGACAT 20

RESULT 3  
 AAAS15192  
 ID AAAS15192 standard; DNA; 20 BP.  
 XX  
 AC AAAS15192;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human bcl-x antisense oligonucleotide ISIS 15999.  
 XX  
 KW Human; antisense oligonucleotide; IL-5R; interleukin-5 receptor; ss;  
 KW antiinfection; antiinflammatory; cytostatic; inflammation; infection;  
 KW tumour; ISIS 15999; probe.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2' methoxyethoxy residues when 16-20 are also 2'  
 FT methoxyethoxy residues. All cytosines in this region are  
 FT also 5-methyl-cytosine"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2' methoxyethoxy residues when 1-5 are also 2'  
 FT methoxyethoxy residues. All cytosines in this region are  
 FT also 5-methyl-cytosine"

WO200172765-A1.

04-OCT-2001.

28-MAR-2000; 2000WO-US008174.

28-MAR-2000; 2000WO-US008174.

(ISIS-) ISIS PHARM INC.

Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;  
 Freier SM, McKay R, Karras JG;

WPI; 2001-626250/72.

Controlling cell behavior, useful e.g. for treatment of tumors, by  
 modulating processing, e.g. splicing, of specific mRNA sequences with non  
 -cleaving antisense agents.

Example 14; Page 83; 121pp; English.

The invention relates to controlling cell behaviour by modulating the  
 processing of a selected wild-type mRNA target in the cell, is new. The  
 mRNA is bound to a specific-binding antisense compound that does not  
 cleave bound mRNA. The antisense oligonucleotides are useful as research  
 reagents, diagnostic agents (in hybridisation assays), and for treatment  
 or prevention of diseases, e.g. to prevent or delay infections,  
 inflammation and tumours. The present sequence is an antisense  
 oligonucleotide which targets the gene for human bcl-x

Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCGTTGCTCTGAGACAT 20
    |||
Db 1 TCCCGTTGCTCTGAGACAT 20
    |||

RESULT 4
AAH27678
ID AAH27678 standard; DNA; 20 BP.
XX
AC AAH27678;
XX
XX
DT 13-AUG-2001 (first entry)
XX
DE Human bcl-x antisense chimeric oligonucleotide SEQ ID 21.
XX
XX Antisense oligonucleotide; bcl-x; human; apoptosis; inflammation; cancer;
KW glioblastoma; leukaemia; autoimmune disorder; Alzheimer's disease;
KW neurodegenerative disorder; AIDS; Parkinson's disease; phosphorothioate;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /mod_base= OTHER
XX /label= Phosphorothioate internucleotide linkage
XX modified_base 1..5
XX /mod_base= b
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyl (2'-MOE) nucleotides, where
XX cytidine residues are 5-methylcytidines"
XX modified_base 16..20
XX /mod_base= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyl (2'-MOE) nucleotides, where
XX cytidine residues are 5-methylcytidines"
XX
XX US2001007025-A1.
XX
XX 05-JUL-2001.
XX
XX 12-DEC-2000; 2000US-00734846.
XX
XX 07-OCT-1998; 98US-00167921.
XX
XX 26-MAR-1999; 99US-00277020.
XX
XX 02-JUN-1999; 99US-00223743.
XX
XX (BENN/) BENNETT C F.
XX (DEAN/) DEAN N M.
XX (MONI/) MONIA B P.
XX (NICK/) NICKLOFF B J.
XX (ZHAN/) ZHANG Q Q.
XX
XX Bennett CF, Dean NM, Monia BP, Nickloff BJ, Zhang QQ;
XX WPI; 2001-397228/42.
XX
XX Antisense compound, 8 to 30 nucleobases in length, targeted to a nucleic
XX acid molecule encoding a human bcl-x, useful for preventing or treating
XX tumor formation, infection or inflammation.
XX
XX Example 16; Page 17; 47pp; English.
XX
XX This invention relates to antisense oligonucleotides which are between 8
XX and 30 nucleobases in length and are targeted to a nucleotide sequence
XX encoding human bcl-x. Human Bcl-x functions as a bcl-2-independent

```

---

```

CC regulator of apoptosis. The invention includes a method of inhibiting the
CC expression of bcl-x in human cells or tissues through antisense
CC inhibition by the antisense oligonucleotides. An antisense compound
CC containing the oligonucleotide together with a chemotherapeutic agent is
CC useful for preventing or treating tumour formation. The antisense
CC compound is also useful for treating or preventing infection or
CC inflammation. Cancer particularly glioblastoma and leukaemia, autoimmune
CC disorders and viral infections, AIDS, neurodegenerative disorders like
CC Alzheimer's or Parkinson's diseases may be treated using compounds
CC containing the antisense oligonucleotides. The present sequence
CC represents an antisense oligonucleotide targeted against a region of the
CC human bcl-x gene
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match      100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCGTTGCTCTGAGACAT 20
    |||
Db 1 TCCCGTTGCTCTGAGACAT 20
    |||

RESULT 5
ABV73650
ID ABV73650 standard; DNA; 20 BP.
XX
AC ABV73650;
XX
XX 06-JAN-2003 (first entry)
XX
XX Human bcl-x exon 1/exon 2 antisense oligonucleotide #SEQ ID 42.
XX
XX Antisense therapy; antisense oligonucleotide; apoptosis; mitosis;
XX differentiation; stress; hormone; cytokine; signalling molecule;
XX mRNA modulation; mRNA cleavage; therapeutic; human; bcl-x; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /mod_base= a
XX /note= "nucleotides 1-5 and 16-20 are 2'-methoxyethoxy
XX (2'-MOE); all 2'-MOE cytosines are 5-methyl-cytosines; all
XX linkages are phosphorothioate"
XX
XX US2002049173-A1.
XX
XX 25-APR-2002.
XX
XX 12-DEC-2000; 2000US-00734847.
XX
XX 26-MAR-1999; 99US-00277020.
XX
XX (BENN/) BENNETT C F.
XX (CROO/) CROOKE S T.
XX (MANO/) MANOHARAN M.
XX (WYAT/) WYATT J.
XX (BAKE/) BAKER B F.
XX (MONI/) MONIA B P.
XX (MCKA/) MCKAY R.
XX (KARR/) KARRAS J G.
XX
XX Bennett CF, Crooke ST, Manoharan M, Wyatt J, Baker BP, Monia BP;
XX McKay R, Karras JG;
XX WPI; 2002-415043/44.
XX
XX Controlling cell behavior by modulating mRNA modification, useful in
XX therapeutics and as research tool, comprises using antisense
XX oligonucleotide which hybridize to mRNA and block modification regions

```

PT such as splice acceptor sites.

XX Example 14; Page 28; 50pp; English.

XX The invention relates to the control of cell behaviour by modulating the processing of a wild-type mRNA target, comprising binding to the target an antisense compound which specifically hybridises to the target and does not elicit cleavage of the mRNA upon binding. The method of the invention can be used in therapeutics (i.e. antisense therapy), including prophylaxis, and as a research tool. It is used for controlling the behaviour of a cell (especially responses such as apoptosis, mitosis, differentiation and quiescence to stimuli such as stress, hormones, cytokines and other signalling molecules), tissue or organism through antisense modulation of mRNA processing. The current sequence represents a human bcl-x exon 1/exon 2 antisense oligonucleotide designated SEQ ID 42, designed to target areas of exon 1 and exon 2 of human bcl-x, particularly around the exon 1/exon 2 splice site and in sequence regions present in bcl-x1 but not bcl-x2.

XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||

Db 1 TCCCGGTTGCTCTGAGACAT 20  
|||||

RESULT 6

AD24239

ID ADA24239 standard; DNA; 20 BP.

AC ADA24239;

XX 20-NOV-2003 (first entry)

DE Human bcl-x1 antisense oligonucleotide MB-006 SEQ ID NO:22.

XX therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein; cytostatic; immunosuppressive; virucide; anti-HIV; antibacterial; cardiant; hyperproliferation; cancer; haematological; metastatic; autoimmune disease; infection; endocrine; neural; cardiovascular; pulmonary; reproductive system disorder; endocytosis; metabolic process; murine; intracellular adhesion molecule 1; ICAM-1; antisense oligonucleotide; phosphorothioate; ss.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "phosphorothioate backbone"

XX WO2003069306-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-US004323.

XX 13-FEB-2002; 2002US-0356053P.

XX (MEDB-) MEDBRIDGE INC.

XX Xie D;

XX WPI; 2003-646491/61.

XX Treating diseases with oligonucleotides or interfering RNA, useful e.g. for cancer or autoimmune diseases, covalently coupled to mobile proteins,

PT in vivo or in vitro.

XX Claim 128; Page 12; 42pp; English.

XX The present invention describes a method for treating a disease by administering: (a) a therapeutic oligonucleotide (TON) or double-stranded RNA (dsRNA) that includes a reactive group (RG) that can react with a mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or (b) TON or dsRNA already conjugated to MP through a covalent bond. Also described: (1) TON of 15-30 bases that includes (i) a part that binds to target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a part that binds to target RNA or DNA and is conjugated to MP through a covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is conjugated to MP through a covalent link. TON have cytostatic, immunosuppressive, virucide, anti-HIV, antibacterial and cardiant activities. The method is used to treat, or prevent, hyperproliferation (particularly cancers, solid or haematological, including prevention of metastatic spread); autoimmune diseases; viral or bacterial infections; endocrine, neural, cardiovascular, pulmonary or reproductive system disorders. Also where TON or dsRNA are labelled, they can be used for diagnosis and monitoring of therapy. When linked to a mobile protein, TON/dsRNA have better cell entry (via endocytosis or other parts of the mobile protein metabolic process) and longer therapeutic life, increased from hours to weeks (the result of increased resistance to nuclease), without loss of affinity for the target. In many cases immune response to TON/dsRNA is also reduced, as is non-specific binding to endogenous proteins. The present sequence represents a human bcl-x1 antisense oligonucleotide, which is a specifically claimed TON from the present invention.

XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
|||||

Db 1 TCCCGGTTGCTCTGAGACAT 20  
|||||

RESULT 7

AD64206

ID AAD64206 standard; DNA; 20 BP.

XX AAD64206;

AC AAD64206;

XX 12-FEB-2004 (first entry)

DE Human bcl-x antisense oligonucleotide ISIS #15999.

XX Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia; retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; acquired immune deficiency syndrome; neurodegenerative disorder; AIDS; neurotropic; anticonvulsant; vasotropic; therapy; cerebroprotective; stroke; antisense; phosphorothioate backbone; ss.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified\_base 1..5

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All cytidines are 5-methyl cytidines"

FT modified\_base 16..20

FT /\*tag= c

```

FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
FT      cytidines are 5-methyl cytidines"
PN      US2003191300-A1.
XX      09-OCT-2003.
XX
XX      21-NOV-2002; 2002US-00302262.
XX
XX      07-OCT-1998; 98US-00167921.
XX      26-MAR-1999; 99US-00277020.
XX      02-JUN-1999; 99US-00323743.
XX      12-DEC-2000; 2000US-00734846.
XX
XX      (BENN/) BENNETT C F.
XX      (DEAN/) DEAN N M.
XX      (MONI/) MONIA B P.
XX      (NICK/) NICKOLOFF B J.
XX      (ZHAN/) ZHANG Q Q.
XX
XX      Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
XX      WPI; 2003-864192/80.
XX
XX      Compound useful for treating reduced apoptotic conditions e.g. cancer
XX      comprises nucleobases targeted to nucleic acid molecule encoding human
XX      gene encoding intracellular membrane protein.
XX
XX      Example 18; SEQ ID NO 21; Opp; English.
XX
XX      The present invention relates to methods for modulating the expression of
XX      bcl-x. The invention is useful for sensitising cancer cells such as
XX      glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
XX      radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
XX      is useful for treating acquired immune deficiency syndrome (AIDS),
XX      neurodegenerative disorders such as Alzheimer's disease, Parkinson's
XX      disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
XX      and ischaemia such as myocardial infarction and stroke. The present
XX      sequence is human bcl-x antisense oligonucleotide
XX
XX      Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 10; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1 TCCCGGTTGCTCTGAGACAT 20
XX      |||||||
XX      Db      1 TCCCGGTTGCTCTGAGACAT 20
XX
XX      RESULT 8
XX      AAD64265
XX      ID      AAD64265 standard; DNA; 20 BP.
XX      AC      AAD64265;
XX      XX
XX      12-FEB-2004 (first entry)
XX
XX      Human bcl-x antisense oligonucleotide ISIS #17959.
XX
XX      Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
XX      retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;
XX      Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX      acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;
XX      nototropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
XX      stroke; antisense; phosphorothioate backbone; ss.
XX
XX      Homo sapiens.
XX      OS      Synthetic.
XX      XX
XX      Key      Location/Qualifiers

```

```

FT      modified_base 1. 20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone"
FT      modified_base 11. 20
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
FT      cytosines are 5-methyl cytosines (5meC)"
XX
XX      US2003191300-A1.
XX
XX      09-OCT-2003.
XX
XX      21-NOV-2002; 2002US-00302262.
XX
XX      07-OCT-1998; 98US-00167921.
XX      26-MAR-1999; 99US-00277020.
XX      02-JUN-1999; 99US-00323743.
XX      12-DEC-2000; 2000US-00734846.
XX
XX      (BENN/) BENNETT C F.
XX      (DEAN/) DEAN N M.
XX      (MONI/) MONIA B P.
XX      (NICK/) NICKOLOFF B J.
XX      (ZHAN/) ZHANG Q Q.
XX
XX      Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;
XX      WPI; 2003-864192/80.
XX
XX      Compound useful for treating reduced apoptotic conditions e.g. cancer
XX      comprises nucleobases targeted to nucleic acid molecule encoding human
XX      gene encoding intracellular membrane protein.
XX
XX      Example 21; Page 19; Opp; English.
XX
XX      The present invention relates to methods for modulating the expression of
XX      bcl-x. The invention is useful for sensitising cancer cells such as
XX      glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet
XX      radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention
XX      is useful for treating acquired immune deficiency syndrome (AIDS),
XX      neurodegenerative disorders such as Alzheimer's disease, Parkinson's
XX      disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy
XX      and ischaemia such as myocardial infarction and stroke. The present
XX      sequence is human bcl-x antisense oligonucleotide. This sequence is the
XX      analogue of ISIS 15999
XX
XX      Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 10; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1 TCCCGGTTGCTCTGAGACAT 20
XX      |||||||
XX      Db      1 TCCCGGTTGCTCTGAGACAT 20
XX
XX      RESULT 9
XX      AAD64264
XX      ID      AAD64264 standard; DNA; 20 BP.
XX      XX
XX      AC      AAD64264;
XX      XX
XX      12-FEB-2004 (first entry)
XX
XX      Human bcl-x antisense oligonucleotide ISIS #17958.
XX
XX      Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
XX      retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;
XX      Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX      acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;

```

KW nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective;  
 KW stroke; antisense; phosphorothioate backbone; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT modified\_base 1..10  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All  
 FT cytosines are 5-methyl cytosines (5mC)"  
 XX  
 PN US2003191300-A1.  
 XX  
 XX  
 PD 09-OCT-2003.  
 XX  
 XX 21-NOV-2002; 2002US-00302262.  
 XX  
 XX 07-OCT-1998; 98US-00167921.  
 PR 26-MAR-1999; 99US-00277020.  
 PR 02-JUN-1999; 99US-00323743.  
 PR 12-DEC-2000; 2000US-00734846.  
 XX  
 XX (BENN/) BENNETT C F.  
 PA (DEAN/) DEAN N M.  
 PA (MONI/) MONIA B P.  
 PA (NICK/) NICKOLOFF B J.  
 PA (ZHAN/) ZHANG Q Q.  
 XX  
 XX Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;  
 PI WPI; 2003-864192/80.  
 DR  
 XX Compound useful for treating reduced apoptotic conditions e.g. cancer  
 FT comprises nucleobases targeted to nucleic acid molecule encoding human  
 FT gene encoding intracellular membrane protein.  
 XX  
 XX Example 21; Page 19; Opp; English.  
 XX  
 CC The present invention relates to methods for modulating the expression of  
 CC bcl-x. The invention is useful for sensitising cancer cells such as  
 CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet  
 CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention  
 CC is useful for treating acquired immune deficiency syndrome (AIDS),  
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy  
 CC and ischaemia such as myocardial infarction and stroke. The present  
 CC sequence is human bcl-x antisense oligonucleotide. This sequence is the  
 CC analogue of ISIS 15999  
 XX  
 XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCCGGTTGCTTGACAT 20  
 |||||  
 DB 1 TCCCGGTTGCTTGACAT 20  
 |||||  
 RESULT 10  
 AAD64263  
 ID AAD64263 standard; DNA; 20 BP.  
 XX  
 AC AAD64263;  
 XX  
 DT 12-FEB-2004 (first entry)

XX Human bcl-x antisense oligonucleotide ISIS #17791.  
 DE  
 XX  
 KW Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;  
 KW retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic;  
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW acquired immune deficiency syndrome; neurodegenerative disorder; AIDS;  
 KW nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective;  
 KW stroke; antisense; phosphorothioate backbone; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All  
 FT cytosines are 5-methyl cytosines (5mC)"  
 FT modified\_base 5..16  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All  
 FT cytosines are 5-methyl cytosines (5mC)"  
 XX  
 PN US2003191300-A1.  
 XX  
 XX 09-OCT-2003.  
 PD  
 XX 21-NOV-2002; 2002US-00302262.  
 XX  
 XX 07-OCT-1998; 98US-00167921.  
 PR 26-MAR-1999; 99US-00277020.  
 PR 02-JUN-1999; 99US-00323743.  
 PR 12-DEC-2000; 2000US-00734846.  
 XX  
 XX (BENN/) BENNETT C F.  
 PA (DEAN/) DEAN N M.  
 PA (MONI/) MONIA B P.  
 PA (NICK/) NICKOLOFF B J.  
 PA (ZHAN/) ZHANG Q Q.  
 XX  
 XX Bennett CF, Dean NM, Monia BP, Nickoloff BJ, Zhang QQ;  
 PI WPI; 2003-864192/80.  
 DR  
 XX Compound useful for treating reduced apoptotic conditions e.g. cancer  
 FT comprises nucleobases targeted to nucleic acid molecule encoding human  
 FT gene encoding intracellular membrane protein.  
 XX  
 XX Example 21; Page 19; Opp; English.  
 XX  
 CC The present invention relates to methods for modulating the expression of  
 CC bcl-x. The invention is useful for sensitising cancer cells such as  
 CC glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet  
 CC radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention  
 CC is useful for treating acquired immune deficiency syndrome (AIDS),  
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy  
 CC and ischaemia such as myocardial infarction and stroke. The present  
 CC sequence is human bcl-x antisense oligonucleotide. This sequence is the  
 CC analogue of ISIS 15999  
 XX  
 XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 TCCCGGTGCTCTGAGACAT 20  
|  
Db 1 TCCCGGTGCTCTGAGACAT 20  
|  
RESULT 11  
AAV57313/C  
ID AAV57313 standard; DNA; 30 BP.  
XX AC AAV57313;  
XX DT 19-NOV-1998 (first entry)  
XX DE 5' primer, used to amplify bcl-xL cDNA.  
XX KW Primer; PCR; amplification; bcl-xL; cell death suppressing gene; pM21;  
XX KW pBluescript; stress-resistant plant; UV irradiation; high salinity;  
XX KW superoxide-generating herbicide; ss.  
XX OS Synthetic.  
XX OS Homo sapiens.  
XX PN EP864650-A2.  
XX PD 16-SEP-1998.  
XX PF 11-MAR-1998; 98EP-00301786.  
XX PR 11-MAR-1997; 97JP-00056743.  
XX PR 19-JAN-1998; 98JP-00080856.  
XX PA (NORU) NAT INST AGROBIOLOGICAL RESOURCES MIN.  
XX PI Ohashi Y, Mitsuhashi I, Malik KA;  
XX DR WPI; 1998-469234/41.  
XX PT New stress-resistant transgenic plants, comprise cell death suppressing  
PT gene - used to confer resistance to stress caused by UV irradiation,  
PT super-oxide-generating herbicides or high salinity.  
XX PS Example 2; Page 7; 3lpp; English.  
XX CC Primers AAV57313 and AAV57314 were used to amplify the human bcl-xL (cell  
CC death suppressing gene) gene isolated from a human cDNA library. After  
CC amplification, the product was cloned into the EcoRI site of pBluescript,  
CC thus obtaining the plasmid pM21. This plasmid, was used in the  
CC construction of an expression vector which can then be used in the  
CC preparation of a stress-resistant plant, by introducing this gene into a  
CC plant cell and then using this cell to regenerate a plant. The stress-  
CC resistant plants produced by this method have been found to show  
CC increased resistance to stress caused by UV irradiation, superoxide-  
CC generating herbicides or high salinity  
XX SQ Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCCGGTGCTCTGAGACAT 20  
|  
Db 20 TCCCGGTGCTCTGAGACAT 1  
|  
RESULT 12  
AAH43465/C  
ID AAH43465 standard; DNA; 31 BP.;  
XX AC AAH43465;  
XX DT 04-DEC-2001 (first entry)  
XX DE 5' primer, used to amplify bcl-xL cDNA.  
XX KW random oligonucleotide library; protein interaction; ligand;  
XX KW receptor binding site; PCR; primer; ss; human;  
XX KW apoptosis inhibitory factor; Bcl-XL.  
XX OS Homo sapiens.  
XX PN JP2004024078-A.  
XX PD 29-JAN-2004.  
XX PF 24-JUN-2002; 2002JP-00183456.  
DE cDNA clone HP03564 ORF, primer P1.  
XX NW38; NPWP; protein interaction; reporter function; eukaryotic cell;  
KW localization; protein network; intracellular; primer; amplify; PCR;  
KW polymerase chain reaction; mitochondria; ss.  
XX OS Synthetic.  
XX OS WO200168885-A1.  
XX PN 20-SEP-2001.  
XX PD 13-MAR-2001; 2001WO-JP001973.  
XX PF 15-MAR-2000; 2000JP-00073095.  
XX PR 24-AUG-2000; 2000JP-00254418.  
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX PI Kato S, Eguchi C, Nagata N, Otake M;  
XX DR WPI; 2001-590069/66.  
XX PT Detection of protein-protein interactions for screening compounds capable  
PT of modifying the interaction comprises observing intracellular  
PT localization of one protein after altering the modification pattern.  
XX PS Example 6; Page 30; 33pp; Japanese.  
XX CC The sequences given in AAH43465-67 are primers which were used to amplify  
CC the open reading frame of the mitochondrial cDNA clone HP03564. The  
CC protein encoded by the amplified sequence was used in the method of the  
CC invention. The method allows detection of interactions between a protein  
CC X and a protein Y which has a reporter function in eukaryotic cells, and  
CC comprises modifying the localization patterns of X and/or Y, and the  
CC localization of Y in the cell is observed using the reporter function.  
CC This method is useful for the elucidation of protein networks within the  
CC cell. It is also applicable for the discovery of new proteins and low-  
CC molecular drugs, by observing their effect on intracellular protein  
CC interactions  
XX SQ Sequence 31 BP; 8 A; 8 C; 11 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 5; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCCGGTGCTCTGAGACAT 20  
|  
Db 30 TCCCGGTGCTCTGAGACAT 11  
|  
RESULT 13  
ADM45992/C  
ID ADM45992 standard; DNA; 31 BP.  
XX AC ADM45992;  
XX DT 03-JUN-2004 (first entry)  
XX DE Primer 1 used to amplify human apoptosis inhibitory factor Bcl-xL cDNA.  
XX KW random oligonucleotide library; protein interaction; ligand;  
XX KW receptor binding site; PCR; primer; ss; human;  
XX KW apoptosis inhibitory factor; Bcl-XL.  
XX OS Homo sapiens.  
XX PN JP2004024078-A.  
XX PD 29-JAN-2004.  
XX PF 24-JUN-2002; 2002JP-00183456.

XX 24-JUN-2002; 2002JP-00183456.  
PR (SERE-) SERESUTA REKISHIKO SCI KK.  
PA WPI; 2004-161478/16.  
XX  
XX Random oligonucleotide useful for detecting protein interaction, having  
PT base sequence, where each base of 1st and 2nd of the codon is the any of  
PT G, C,T (U), or A and the base of 3rd of codon is G or C, or G or T (U).  
XX  
XX Example 2; SEQ ID NO 1; 43pp; Japanese.  
XX  
XX The invention relates to a novel random oligonucleotide having a base  
CC sequence where each base of the 1st and 2nd codon is any of G, C, T (U)  
CC or A and each base of the 3rd codon is G or C, or G or T (U). The methods  
CC of the invention may be useful for preparing a random oligonucleotide  
CC preparation to be used for detecting protein interactions or for  
CC screening ligand or receptor protein binding sites. The current sequence  
CC is that of the PCR primer 1 of the invention which was used to amplify  
CC human apoptosis inhibitory factor Bcl-XL cDNA.  
XX  
SQ Sequence 31 BP; 7 A; 10 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCCGGTGCTCTGAGACAT 20  
Db 29 TCCCGGTGCTCTGAGACAT 10  
RESULT 14  
ADH52648/c  
ID ADH52648 standard; DNA; 37 BP.  
XX  
AC ADH52648;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE RT-PCR primer Eco-Bcl used to amplify Chinese hamster bcl-xL RNA.  
XX  
XX mammalian myeloma host cell; protein production; anti-apoptosis;  
KW cell death; Chinese hamster; bcl-xL; PCR; primer; ss; RT-PCR.  
XX  
OS Synthetic.  
OS Cricetulus griseus.  
XX  
PN US2003219871-A1.  
XX  
PD 27-NOV-2003.  
XX  
PF 28-MAR-2003; 2003US-00402017.  
XX  
PR 02-APR-2002; 2002US-0369307P.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.  
XX  
PI Enkel B, Meents H, Fussenegger M;  
XX  
XX WPI; 2004-033642/03.  
DR  
XX New genetically engineered hamster or murine myeloma host cells  
PT comprising enhanced levels of active anti-apoptosis genes, useful for  
PT producing complex protein therapeutics.  
XX  
XX Example 5; SEQ ID NO 19; 46pp; English.  
XX  
XX The invention relates to a novel mammalian host cell for producing  
CC protein therapeutics. The host cell comprises a hamster or a murine  
CC myeloma cell that is genetically modified by introduction of nucleic acid  
CC sequences encoding an anti-apoptosis gene, a selectable amplifiable  
XX  
CC marker gene and at least one gene of interest. The host cell of the  
CC invention may be useful for producing at least one protein encoded by a  
CC gene of interest. The DNA, polypeptide and the methods may be used for  
CC inhibiting or delaying cell death. The current sequence is that of the  
CC Chinese hamster anti-apoptosis bcl-xL-related PCR primer which was used  
CC in the exemplification of the invention.  
XX  
SQ Sequence 37 BP; 9 A; 12 C; 10 G; 6 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCCGGTGCTCTGAGACAT 20  
Db 36 TCCCGGTGCTCTGAGACAT 17  
RESULT 15  
AAT40080/c  
ID AAT40080 standard; cDNA; 39 BP.  
XX  
AC AAT40080;  
XX  
DT 30-MAR-1997 (first entry)  
XX  
DE Primer for bcl-XS open reading frame amplification by PCR.  
XX  
XX Primer; bcl-XS; PCR; polymerase chain reaction; bcl-XL; T-lymphocyte;  
KW activation; cell death; antibody; CD28 costimulation; gene therapy; HIV;  
KW AIDS; antisense; immune disorder; autoimmune disease; graft rejection;  
KW graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO9634956-A1.  
XX  
PD 07-NOV-1996.  
XX  
PF 02-MAY-1996; 96WO-US006203.  
XX  
PR 04-MAY-1995; 95US-00435518.  
PR 07-JUN-1995; 95US-00481739.  
XX  
PA (USNA ) US SEC OF NAVY.  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI June CH, Thompson CB;  
XX  
DR WPI; 1996-506159/50.  
XX  
PT Inducing or preventing death of T cells by bcl-XL protein regulation -  
PT used to increase survival of HIV infected cells or to down-regulate  
PT immune responses in immune diseases.  
XX  
PS Example 5; Page 38; 76pp; English.  
XX  
XX This primer may be used with AAT40081 in PCR to amplify the bcl-XS (short  
CC form splice variant) open reading frame in the bcl-X gene, which also  
CC encodes a long form (bcl-XL) protein. Bcl-XL protein protects T-  
CC lymphocytes against cell death, and bcl-XS is a dominant regulator. The  
CC amplified bcl-XS fragment has been cloned into NdeI and BamHI sites of  
CC plasmid pBT-3b, and expressed in BL21 cells, for use in generation of  
CC rabbit polyclonal antibodies and mouse monoclonal antibodies to monitor  
CC bcl-XL and bcl-XS protein levels in T-cells. Immunoassays using the  
CC antibodies have shown that resting T-cells do not express bcl-XL, whereas  
CC anti-CD3- activated T-cells express the protein, and expression levels  
CC are increased by anti-CD28 costimulation. The bcl-XL gene may be  
CC introduced into T-cells in vivo or ex vivo for HIV infection gene  
CC therapy, or may be introduced in antisense orientation for gene therapy  
CC of autoimmune disease, graft rejection or graft-versus-host disease  
XX Sequence 39 BP; 11 A; 7 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20  
 |||||  
 Db 32 TCCCGGTGCTCTGAGACAT 13

Search completed: February 4, 2005, 21:52:37  
 Job time : 260.033 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-2  
Perfect score: 20  
Sequence: 1 tcccggtgtctgagacat 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gsl1.\*  
9: gb\_gsl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	119	2	BE796096
C 2	20	100.0	129	2	BE275197
C 3	20	100.0	136	9	CG608749
C 4	20	100.0	151	2	BE386533
C 5	20	100.0	162	4	BM050693
C 6	20	100.0	177	2	BF688810
C 7	20	100.0	200	1	AA351198
C 8	20	100.0	210	4	BG334446
C 9	20	100.0	213	4	BG478819
C 10	20	100.0	218	4	BG752203
C 11	20	100.0	223	2	BE727284
C 12	20	100.0	225	2	BF026532
C 13	20	100.0	227	2	BE275637
C 14	20	100.0	230	2	BF685843
C 15	20	100.0	232	4	BG746689
C 16	20	100.0	239	2	BE728507
C 17	20	100.0	248	2	BE386614
C 18	20	100.0	251	2	BE269450
C 19	20	100.0	251	4	BM049633
C 20	20	100.0	252	2	BE560320
C 21	20	100.0	262	4	BG479739
C 22	20	100.0	275	4	BM012517
C 23	20	100.0	297	2	BF128036
C 24	20	100.0	301	4	BG419161
C 1	20	100.0	119	2	BE796096
C 2	20	100.0	129	2	BE275197
C 3	20	100.0	136	9	CG608749
C 4	20	100.0	151	2	BE386533
C 5	20	100.0	162	4	BM050693
C 6	20	100.0	177	2	BF688810
C 7	20	100.0	200	1	AA351198
C 8	20	100.0	210	4	BG334446
C 9	20	100.0	213	4	BG478819
C 10	20	100.0	218	4	BG752203
C 11	20	100.0	223	2	BE727284
C 12	20	100.0	225	2	BF026532
C 13	20	100.0	227	2	BE275637
C 14	20	100.0	230	2	BF685843
C 15	20	100.0	232	4	BG746689
C 16	20	100.0	239	2	BE728507
C 17	20	100.0	248	2	BE386614
C 18	20	100.0	251	2	BE269450
C 19	20	100.0	251	4	BM049633
C 20	20	100.0	252	2	BE560320
C 21	20	100.0	262	4	BG479739
C 22	20	100.0	275	4	BM012517
C 23	20	100.0	297	2	BF128036
C 24	20	100.0	301	4	BG419161

C 25	20	100.0	320	5	BY220922
C 26	20	100.0	323	5	BY329071
C 27	20	100.0	325	5	BY191347
C 28	20	100.0	326	5	BY181507
C 29	20	100.0	327	5	BY209882
C 30	20	100.0	336	5	BY219527
C 31	20	100.0	341	5	BY176914
C 32	20	100.0	344	2	BB869154
C 33	20	100.0	348	5	BY010071
C 34	20	100.0	350	5	BY058101
C 35	20	100.0	353	5	BY016163
C 36	20	100.0	355	5	BY180189
C 37	20	100.0	355	5	BY212491
C 38	20	100.0	356	6	CB113589
C 39	20	100.0	357	2	BB870590
C 40	20	100.0	358	5	BY203613
C 41	20	100.0	361	5	BY176753
C 42	20	100.0	363	5	BY221240
C 43	20	100.0	363	5	BY293078
C 44	20	100.0	367	2	BB843018
C 45	20	100.0	367	2	BB843018

#### ALIGNMENTS

RESULT 1  
BE796096/c  
LOCUS BE796096 119 bp mRNA linear EST 20-SEP-2000  
DEFINITION 601590910F1 NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:3944786 5',  
mRNA sequence.  
ACCESSION BE796096  
VERSION BE796096.1 GI:10217294  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE NTH-MGC http://mgc.nci.nih.gov/  
AUTHORS 1 (bases 1 to 119)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L1CM802 row: d column: 03  
High quality sequence start: 25  
High quality sequence stop: 119.  
Location/Qualifiers  
1. 119  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3944786"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
ORIGIN



/tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_20"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20  
 ||||||||||||||||  
 Db 123 TCCCGGTGCTCTGAGACAT 104

## RESULT 5

BM050693/c  
 LOCUS 603633458F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:5423943 5',  
 DEFINITION mRNA sequence.

ACCESSION BM050693

VERSION BM050693.1 GI:16779960

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 162)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LUCM1884 row: c column: 16

High quality sequence stop: 162.

Location/Qualifiers

## FEATURES

source

1. 162  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5423943"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20

Db 114 TCCCGGTGCTCTGAGACAT 95  
 ||||||||||||||||

## RESULT 6

BF688810/c

LOCUS 602184995F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4299479 5',  
 DEFINITION mRNA sequence.

ACCESSION BF688810

VERSION BF688810.1 GI:11974218

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 177)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LUCM1156 row: n column: 24

High quality sequence start: 2

High quality sequence stop: 177.

Location/Qualifiers

## FEATURES

source

1. 177  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4299479"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20  
 ||||||||||||||||  
 Db 129 TCCCGGTGCTCTGAGACAT 110

## RESULT 7

AA351198/c

LOCUS AA351198

DEFINITION EST58853 Infant brain Homo sapiens cDNA 5' end similar to apoptosis  
 regulator bcl-x, mRNA sequence.

ACCESSION AA351198

VERSION AA351198.1 GI:2003517

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 200)

**AUTHORS.** Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.  
**TITLE** Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library  
**JOURNAL** Nat. Genet. 4, 373-380 (1993)  
**MEDLINE** 94004965  
**PUBMED** 8401585  
**COMMENT** Other ESTs: THC105965  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

**FEATURES** source  
 Location/Qualifiers  
 1..200

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="ATCC (inhost):151593"  
/db\_xref="taxon:9606"  
/sex="female"  
/dev\_stage="infant"  
/clone\_lib="Infant brain"  
/notes="Organ: brain; Vector: lafmid BA; Site\_1: HindIII; Site\_2: NotI"

**ORIGIN**

Query Match 100.0%; Score 20; DB 1; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
 |||||  
 Db 179 TCCCGGTTGCTCTGAGACAT 160

**RESULT 8**  
 BG334446/c  
**LOCUS** BG334446 210 bp mRNA linear EST 27-FEB-2001  
**DEFINITION** 602461986F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4578596 5', mRNA sequence.

**ACCESSION** BG334446  
**VERSION** BG334446.1 GI:13140884  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE** 1 (bases 1 to 210)  
**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCML294 row: 1 column: 21  
 High quality sequence stop: 210.

**FEATURES** source  
 Location/Qualifiers  
 1..210  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4578596"

/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_20"  
/notes="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**ORIGIN**

Query Match 100.0%; Score 20; DB 4; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20  
 |||||  
 Db 162 TCCCGGTTGCTCTGAGACAT 143

**RESULT 9**

BG478819/c

**LOCUS** BG478819

**DEFINITION** 602525369F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4643800 5', mRNA sequence.

**ACCESSION** BG478819

**VERSION** BG478819.1 GI:13411098

**KEYWORDS** EST.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE** 1 (bases 1 to 213)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)

**JOURNAL** Unpublished (1999)

**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCM1414 row: 1 column: 17  
 High quality sequence stop: 213.

**FEATURES** source  
 Location/Qualifiers  
 1..213  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4643800"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_20"  
/notes="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**ORIGIN**

Query Match 100.0%; Score 20; DB 4; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTTGCTCTGAGACAT 20



```

Db      165  TCCCGGTGCTCTGAGACAT 146
|||||
RESULT 10
BG752203/c
LOCUS
DEFINITION 602731335F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874865 5',
mRNA sequence.
ACCESSION BG752203
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 218)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1755 row: e column: 10
High quality sequence stop: 218.
Location/Qualifiers
1..218
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4874865"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

FEATURES
source
Query Match 100.0%; Score 20; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCGGTGCTCTGAGACAT 20
|||||
Db 170 TCCCGGTGCTCTGAGACAT 151
|||||

RESULT 11
BE727284/c
LOCUS
DEFINITION 601560967F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830416 5',
mRNA sequence.
ACCESSION BE727284
VERSION BE727284.1 GI:10141377
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 223)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM829 row: n column: 22
High quality sequence stop: 225.
Location/Qualifiers
1..225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM504 row: f column: 17
High quality sequence start: 38
High quality sequence stop: 223.
Location/Qualifiers
1..223
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3830416"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

/clone="IMAGE:3955413"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTGCTCTGAGACAT 20  
|||||  
Db 197 TCCCGGTGCTCTGAGACAT 178  
|||||

RESULT 13  
BE275637/c  
LOCUS BE275637 227 bp mRNA linear EST 13-JUL-2000  
DEFINITION 601121162F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:2988806 5',  
mRNA sequence.  
ACCESSION BE275637  
VERSION BE275637.1 GI:9150595  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 227)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM78 row: k column: 15  
High quality sequence start: 27  
High quality sequence stop: 227.  
Location/Qualifiers

FEATURES  
source  
1..227  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2988806"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_20"  
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTGCTCTGAGACAT 20  
|||||  
Db 199 TCCCGGTGCTCTGAGACAT 180  
|||||

RESULT 14  
BF685843/c  
LOCUS BF685843 230 bp mRNA linear EST 22-DEC-2000  
DEFINITION 602143136F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4304288 5',  
mRNA sequence.  
ACCESSION BF685843  
VERSION BF685843.1 GI:11971251  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 230)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM169 row: g column: 09  
High quality sequence stop: 230.  
Location/Qualifiers

FEATURES  
source  
1..230  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4304288"  
/tissue\_type="leiomyosarcoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_46"  
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCGGTGCTCTGAGACAT 20  
|||||  
Db 182 TCCCGGTGCTCTGAGACAT 163  
|||||

RESULT 15  
BG746689/c  
LOCUS BG746689 232 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602704010F1 NTH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4857171 5',  
mRNA sequence.  
ACCESSION BG746689  
VERSION BG746689.1 GI:14057342  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 232)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM169 row: g column: 09  
High quality sequence stop: 230.  
Location/Qualifiers

FEATURES  
source  
1..232  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4857171"  
/tissue\_type="leiomyosarcoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_15"  
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 232)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM1709 row: d column: 04  
High quality sequence stop: 232.

FEATURES  
Location/Qualifiers  
1..232  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4857171"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_15"  
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TCCCGGTTCCTCTGAGACAT 20  
|||||  
Db 184 TCCCGGTTCCTCTGAGACAT 165

Search completed: February 5, 2005, 08:11:25  
Job time : 2386.67 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-3  
Perfect score: 20  
Sequence: 1 gccacagtcgcccgtcag 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235151
2	20	100.0	20	6	BD235165
3	20	100.0	20	6	BD235166
4	20	100.0	60	6	CQ543581
5	20	100.0	127	6	CQ112670
6	20	100.0	127	6	CQ151543
7	20	100.0	127	6	CQ185285
8	20	100.0	127	6	CQ234920
9	20	100.0	127	6	CQ272476
10	20	100.0	127	6	CQ310145
11	20	100.0	127	6	CQ346752
12	20	100.0	387	6	CQ732731
13	20	100.0	513	10	MMU10100
14	20	100.0	513	10	AF136230
15	20	100.0	513	10	AF279286
16	20	100.0	519	4	AF247182
17	20	100.0	537	10	S78284
18	20	100.0	540	6	AX925690
19	20	100.0	541	4	AF245487

c 20	20	100.0	541	4	AF245488
c 21	20	100.0	541	4	AF245489
c 22	20	100.0	587	6	CQ09589
c 23	20	100.0	587	6	CQ138575
c 24	20	100.0	587	6	CQ175406
c 25	20	100.0	587	6	CQ221990
c 26	20	100.0	587	6	CQ259935
c 27	20	100.0	587	6	CQ297711
c 28	20	100.0	587	6	CQ334058
c 29	20	100.0	600	6	AX925692
c 30	20	100.0	636	6	BD097037
c 31	20	100.0	660	6	AX925694
c 32	20	100.0	660	6	AX925696
c 33	20	100.0	699	10	MMBCLXL
c 34	20	100.0	702	6	BD084108
c 35	20	100.0	702	6	BD102202
c 36	20	100.0	702	9	BT007208
c 37	20	100.0	702	10	MMU10101
c 38	20	100.0	702	12	BT008248
c 39	20	100.0	726	10	RNU34963
c 40	20	100.0	726	10	S76513
c 41	20	100.0	737	6	AR054022
c 42	20	100.0	737	6	AR172595
c 43	20	100.0	737	6	IS2012
c 44	20	100.0	737	6	AR371662
c 45	20	100.0	737	6	AR380913

#### ALIGNMENTS

RESULT 1	BD235151	20 bp	DNA	linear	PAT 17-JUL-2003							
LOCUS	Oligonucleotide inhibitors of bcl-xL.											
DEFINITION	Oligonucleotide inhibitors of bcl-xL.											
ACCESSION	BD235151											
VERSION	BD235151.1	GI:33044921										
KEYWORDS	JP 2002519048-A/3.											
SOURCE	synthetic construct											
ORGANISM	synthetic construct											
REFERENCE	artificial sequences.											
AUTHORS	1 (bases 1 to 20)											
TITLE	Stein, C.A.											
JOURNAL	Oligonucleotide inhibitors of bcl-xL											
COMMENT	Patent: JP 2002519048-A 3 02-JUL-2002;											
	THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK											
	OS	Artificial Sequence										
	PN	JP 2002519048-A/3										
	PD	02-JUL-2002										
	PF	02-JUL-1999 JP 2000557839										
	PR	02-JUL-1998 US 09/109614										
	PI	CY A STEIN										
	PC	C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,										
	PC	A61K47/48, A61K48/00, A61P35/00, C12N15/00										
	CC	ANTISENSE OLIGONUCLEOTIDE										
	FH	Key	Location/Qualifiers									
	FT	source	1..20									
	FT	/organism='Artificial Sequence'.										
FEATURES												
source	1..20											
	/organism="synthetic construct"											
	/mol_type="genomic DNA"											
	/db_xref="taxon:32630"											
ORIGIN												
Query Match	100.0%; Score 20; DB 6; Length 20;											
Best Local Similarity	100.0%; Pred. No. 35;											
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
Qy	1 GCCACAGTCATGCCGTCAG 20											

```
Db          1 GCCACAGTCATGCCCGTCAG 20

RESULT 2
BD235165
LOCUS      20 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION  BD235165
VERSION     BD235165.1 GI:33044935
KEYWORDS   JP 2002519048-A/17.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xl
JOURNAL    Patent: JP 2002519048-A 17 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/17
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PI 02-JUL-1998 US 09/109614
           CY A STEIN
           PC
C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PROPYNIL dc
CC PROPYNIL dc
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PROPYNIL dt
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
FH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT modified_base (2)..(3)
FT modified_base (5)..(5)
FT modified_base (8)..(8)
FT modified_base (9)..(9)
FT modified_base (11)..(11)
FT modified_base (13)..(15)
FT modified_base (17)..(17)
FT modified_base (18)..(18)
FT misc_binding (8)..(9)
FT misc_binding (13)..(15)
FT misc_binding (17)..(20)

FEATURES
    source
    1..20
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GCCACAGTCATGCCCGTCAG 20
Db          1 GCCACAGTCATGCCCGTCAG 20

RESULT 4
CQ543581/c
LOCUS      60 bp      DNA
DEFINITION Sequence 13216 from Patent WO0210449.
ACCESSION  CQ543581
VERSION     CQ543581.1 GI:41509845
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE       Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
JOURNAL     Patent: WO 0210449-A 13216 07-FEB-2002;
            Compugen Inc. (US)
FEATURES    Location/Qualifiers
    source
    1..60
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 60;

Db          1 GCCACAGTCATGCCCGTCAG 20
Qy          1 GCCACAGTCATGCCCGTCAG 20

RESULT 3
BD235166
LOCUS      20 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xl.
ACCESSION  BD235166
VERSION     BD235166.1 GI:33044936
KEYWORDS   JP 2002519048-A/18.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xl
JOURNAL    Patent: JP 2002519048-A 18 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/18
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
```

Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 36 GCCACAGTCATGCCCGTCAG 17

RESULT 5  
LOCUS CQ112670 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21529 from Patent WO0157272.  
ACCESSION CQ112670  
VERSION CQ112670.1 GI:41082540  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 21529 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =  
1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:  
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 6  
LOCUS CQ151543 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21565 from Patent WO0157276.  
ACCESSION CQ151543  
VERSION CQ151543.1 GI:41158893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 21565 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL  
= 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN  
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 7  
LOCUS CQ185285 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 16681 from Patent WO0157274.  
ACCESSION CQ185285  
VERSION CQ185285.1 GI:41180300  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human heart  
JOURNAL Patent: WO 0157274-A 16681 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =  
1.6-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:  
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 8  
LOCUS CQ234920 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21759 from Patent WO0157273.  
ACCESSION CQ234920  
VERSION CQ234920.1 GI:41218197  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
(03.10.00)<150> US 60/236,359<151> 27 September 2000  
(27.09.00)<150> US 60/234,687<151> 21 September 2000  
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
Patent: WO 0157273-A 21759 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..127  
/organism="Homo sapiens"

```
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 9
LOCUS      CQ310145      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21250 from Patent WO0186003.
ACCESSION  CQ310145
VERSION     CQ310145.1 GI:41270722
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
            = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
            HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 10
LOCUS      CQ310145      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21250 from Patent WO0186003.
ACCESSION  CQ310145
VERSION     CQ310145.1 GI:41270722
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
            = 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
            HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 11
LOCUS      CQ346752      127 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 20846 from Patent WO0157275.
ACCESSION  CQ346752
VERSION     CQ346752.1 GI:41295823
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
JOURNAL      Patent: WO 0157275-A 20846 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
            source
            1..127
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
            AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
            1.00e-65"

ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 12
LOCUS      CQ732731/c      387 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION Sequence 18665 from Patent WO02068579.
ACCESSION  CQ732731
VERSION     CQ732731.1 GI:42313858
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL      Patent: WO 02068579-A 18665 06-SEP-2002;
            PE Corporation (US)
```



```

FEATURES
  source
    Location/Qualifiers
      1..387
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 347 GCCACAGTCATGCCCGTCAG 328

RESULT 13
MMU10100/c
LOCUS
DEFINITION Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
ACCESSION U10100
VERSION U10100.1 GI:506645
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 513)
AUTHORS Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.
TITLE Cloning and molecular characterization of mouse bcl-x in B and T
  lymphocytes
JOURNAL J. Immunol. 153 (10), 4388-4398 (1994)
MEDLINE 95052604
PUBMED 7963517
REFERENCE
  2 (bases 1 to 513)
AUTHORS Behrens, T.W.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
  Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA

FEATURES
  source
    /organism="Mus musculus"
    /mol_type="mRNA"
    /db_xref="taxon:10090"
    /cell_lines="WSH1 265.1 RNA"
    /note="alternatively spliced transcript of bcl-x long,
      GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDLFLSKYKSGWSQFSDVEENRTAEPEETRE
      RETPSANGNPSHMLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
      RAFSDLSQSLHITPGTAYQSFQDTPFDLYGNNAAESRKQERFNRFLTGTWVAGV
      VLLGSLFSRK"

ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
   |||||
Db 473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  /organism="Mus musculus"
  /mol_type="mRNA"
  /db_xref="taxon:10090"
  /cell_lines="WSH1 265.1 RNA"
  /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
  1..513
    /gene="bcl-x long"
  1..513
    /codon_start=1
    /product="bcl-x
```

```

FEATURES
  source
    Location/Qualifiers
      1..387
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCACAGTCATGCCCGTCAG 20
      |||
Db      347 GCCACAGTCATGCCCGTCAG 328

RESULT 13
MMU10100/c
LOCUS      513 bp      mRNA      linear      ROD 30-NOV-1995
DEFINITION Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
ACCESSION U10100
VERSION U10100.1 GI:506645
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 513)
AUTHORS Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.
TITLE Cloning and molecular characterization of mouse bcl-x in B and T
lymphocytes
JOURNAL J. Immunol. 153 (10), 4388-4398 (1994)
MEDLINE 95052604
PUBMED 7963517
REFERENCE
2 (bases 1 to 513)
AUTHORS Behrens, T.W.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA
FEATURES
  source
    /organism="Mus musculus"
    /mol_type="mRNA"
    /db_xref="taxon:10090"
    /cell_lines="WSH1 265.1 RNA"
    /note="alternatively spliced transcript of bcl-x long,
    GenBank Accession Number U10101"
    1..513
    /gene="bcl-x long"
    1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AA82172.1"
    /db_xref="GI:506646"
    /translation="MSQSNRELVDVFLSKYKQSWQSFVDEENRTAEPEETRE
    RETPSANGNPSHWLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
    RAFSDLSQSLHITPGTAYQSFQDTPVDLYGNNAAESRKQGERFNRWFLTGMTVAGV
    VLLGSLFSRK"
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCACAGTCATGCCCGTCAG 20
      |||
Db      473 GCCACAGTCATGCCCGTCAG 454

gene
CDS
  1..513
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /db_xref="taxon:10116"
    /tissue_type="brain"
    /note="Isolated from an ischemic brain"
    1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AAD33683.1"
    /db_xref="GI:4928687"
    /translation="MSQSNRELVDVFLSKYKQSWQSFVDEENRTAEPEETRE
    RETPSANGNPSHWLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
    RAFSDLSQSLHITPGTAYQSFQDTPVDLYGNNAAESRKQGERFNRWFLTGMTVAGV
    VLLGSLFSRK"
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCACAGTCATGCCCGTCAG 20
      |||
Db      473 GCCACAGTCATGCCCGTCAG 454

RESULT 15
AF279286/c
LOCUS      513 bp      mRNA      linear      ROD 02-JUL-2000
DEFINITION Rattus norvegicus bcl-x short form mRNA, complete cds.
ACCESSION AF279286
VERSION AF279286.1 GI:8896160
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 513)
AUTHORS Cao, G., Chen, J. and Chen, D.
TITLE Bcl-Xs expression and its role in brain ischemia
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 513)
AUTHORS Cao, G., Chen, J. and Chen, D.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2000) Neurology, University of Pittsburgh, 3500
Terrace Street, Pittsburgh, PA 15261, USA
FEATURES
  source
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /strain="Sprague-Dawley"
    /db_xref="taxon:10116"
    /tissue_type="cerebellum"
    /dev_stage="postnatal 1 week"
    1..513
    /codon_start=1
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCACAGTCATGCCCGTCAG 20
      |||
Db      473 GCCACAGTCATGCCCGTCAG 454

RESULT 14
AF136230/c
LOCUS      513 bp      mRNA      linear      ROD 01-JUN-1999
DEFINITION Rattus norvegicus bcl-x short mRNA, complete cds.
ACCESSION AF136230
VERSION AF136230.1 GI:4928687
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 513)
AUTHORS He, X.J., Jin, K.L., Graham, S.H. and Simon, R.P.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1999) Neurology, University of Pittsburgh, 3500
Terrace Street, Pittsburgh, PA 15213, USA
FEATURES
  source
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /strain="Sprague-Dawley"
    /db_xref="taxon:10116"
    /tissue_type="brain"
    /note="Isolated from an ischemic brain"
    1..513
    /codon_start=1
    /product="bcl-x short"
    /protein_id="AAD33683.1"
    /db_xref="GI:4928688"
    /translation="MSQSNRELVDVFLSKYKQSWQSFVDEENRTAEPEETRE
    RETPSANGNPSHWLADSPVNGATGSHSSLDAREVTPMAAVKQALREAGDFELRYR
    RAFSDLSQSLHITPGTAYQSFQDTPVDLYGNNAAESRKQGERFNRWFLTGMTVAGV
    VLLGSLFSRK"
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCACAGTCATGCCCGTCAG 20
      |||
Db      473 GCCACAGTCATGCCCGTCAG 454

```

```

/product="bel-x short form"
/protein_id="AAF81262.1"
/db_xref="GI:8896161"
/translation="MSQSNRELVVDFLSYKLSQKGYWSQFSDVEENRTEAPEETEPE
RTPPSAINGNPSWHLADSPAVRGATGHSSLDAREVIPMAAYKQALREAGDEFELRYR
RAFSDLTSQLHTTPGTAYQSFQDTFVDLYGNNAASERKQGERFNRWFLTGMTVAGV
VLLGSLFSRK"

```

ORIGIN

```

Query Match      100.0%; Score 20; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCCACAGTCATGCCCGTCAG 20
Db      473 GCCACAGTCATGCCCGTCAG 454

```

Search completed: February 4, 2005, 23:30:38  
Job time : 482.738 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169a-3

Perfect score: 20

Sequence: 1 gccacagtcagcccgtag 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	Aaz46973 Bcl-Xl MR
C 2	20	100.0	25	12	Adp14975 Renal cel
C 3	20	100.0	25	12	Adp17304 Renal cel
C 4	20	100.0	60	6	Abn40468 Human spl
5	20	100.0	127	4	Aba72432 Human foe
6	20	100.0	127	4	Aa152843 Probe #21
7	20	100.0	127	4	Aba38215 Probe #16
8	20	100.0	127	4	Aak47008 Human bon
9	20	100.0	127	4	Aak20855 Human bra
10	20	100.0	127	4	Abs46769 Human liv
11	20	100.0	127	6	Abs21259 Human gen
C 12	20	100.0	179	12	Ach84269 Human gen
C 13	20	100.0	299	10	Acd94503 Human col
C 14	20	100.0	337	10	Adk66037 Standard1
C 15	20	100.0	492	9	Ach46093 Human inf
C 16	20	100.0	540	12	Adh52634 Chinese h
C 17	20	100.0	587	4	Aba59891 Human foe
18	20	100.0	587	4	Aa139762 Probe #84
19	20	100.0	587	4	Aa28336 Probe #68
20	20	100.0	587	4	Aak34040 Human bon
21	20	100.0	587	4	Aak08161 Human bra

22	20	100.0	587	4	ABs33839 Human liv
23	20	100.0	587	6	ABs08825 Human gen
C 24	20	100.0	587	12	ACH70569 Human gen
C 25	20	100.0	600	12	ADH52636 Chinese h
C 26	20	100.0	636	4	AAH48169 Mutant bc
C 27	20	100.0	660	12	ADH52638 Chinese h
C 28	20	100.0	660	12	ADH52640 Chinese h
C 29	20	100.0	702	5	AAH43464 cDNA clon
C 30	20	100.0	702	12	ADM45994 Human apo
C 31	20	100.0	737	2	AAQ81699 Human thy
C 32	20	100.0	737	10	ABz83507 Toxicolog
C 33	20	100.0	737	11	ADI32132 Human cdn
C 34	20	100.0	863	12	ADH52632 Chinese h
C 35	20	100.0	926	2	AAQ81698 Human thy
C 36	20	100.0	926	2	AAT40079 Bcl-XL ge
C 37	20	100.0	926	3	AAZ93614 Bcl-x gen
C 38	20	100.0	926	4	AA515189 Human bcl
C 39	20	100.0	926	4	AAC90810 Human Bcl
C 40	20	100.0	926	6	ABK84766 Human cdn
C 41	20	100.0	926	8	ABT16641 Human bcl
C 42	20	100.0	926	10	ADD56779 Human bcl
C 43	20	100.0	926	10	AAD64187 Human bcl
C 44	20	100.0	926	11	ADI32104 Human cdn
C 45	20	100.0	926	12	ADH52630 Human ant

ALIGNMENTS

RESULT 1  
AAZ46973  
ID AAZ46973 standard; DNA; 20 BP.  
XX AC  
AC AAZ46973;  
XX AC  
DT 14-APR-2000 (first entry)  
XX AC  
DE Bcl-Xl mRNA specific antisense oligo C.  
XX AC  
KW Anti-apoptotic protein; bcl-XL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX OS Homo sapiens.  
XX WO200001393-A2.  
XX PD 13-JAN-2000.  
XX PF 02-JUL-1999; 99WO-US015250.  
XX PR 02-JUL-1998; 98US-00109614.  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX Stein CA;  
XX WPI; 2000-137140/12.  
XX PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-XL, useful for reducing bcl-XL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
XX PS Claim 1; Fig 1; 69pp; English.  
XX CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-XL. The oligonucleotides can be introduced into tumour cells to reduce bcl-XL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-XL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-XL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
CC represent antisense oligos specific for the bcl-Xl mRNA  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20

DB 1 GCCACAGTCATGCCCGTCAG 20

## RESULT 2

ADP14975/c

ID ADP14975 standard; DNA; 25 BP.

XX

AC ADP14975;

XX

DT 26-AUG-2004 (first entry)

XX

DE Renal cell carcinoma differentially expressed gene probe #1380.

XX

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KX head/neck cancer; differential expression; probe.

XX

OS Homo sapiens.

XX

PN WO2004048933-A2.

XX

PD 10-JUN-2004.

XX

PF 21-NOV-2003; 2003WO-US037481.

XX

XX 21-NOV-2002; 2002US-0427982P.

PR

03-APR-2003; 2003US-0459782P.

XX

XX (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX

PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX

XX WPI; 2004-460799/43.

XX

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX

XX Disclosure; SEQ ID NO 1711; 350pp; English.

XX

XX The invention relate to a method of diagnosing (M1) non-blood disease

CC such as solid tumor by providing peripheral blood sample of human having

CC non-blood disease, and comparing an expression profile of specific genes

CC in the peripheral blood sample to reference expression profile of the

CC genes, where each of the genes is differentially expressed in peripheral

CC blood mononuclear cells (PBMCs) of patients having the disease as

CC compared to PBMCs of normal humans. The method is useful for diagnosing

CC non-blood disease such as solid tumor. The solid tumor is chosen from

CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The

CC peripheral blood sample comprises enriched PBMCs. The peripheral blood

CC sample is a whole blood sample (claimed). (M1) is useful for identifying

CC genes that are differentially expressed in peripheral blood samples

CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to

CC detect a gene that is differentially expressed and detected by the method

CC of the invention.

XX Sequence 25 BP; 3 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;

Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20

DB 23 GCCACAGTCATGCCCGTCAG 4

## RESULT 3

ADP17304/c

ID ADP17304 standard; DNA; 25 BP.

XX

AC ADP17304;

XX

DT 26-AUG-2004 (first entry)

XX

DE Renal cell carcinoma differentially expressed gene probe #3709.

XX

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KX head/neck cancer; differential expression; probe.

XX

OS Homo sapiens.

XX

PN WO2004048933-A2.

XX

PD 10-JUN-2004.

XX

PF 21-NOV-2003; 2003WO-US037481.

XX

XX 21-NOV-2002; 2002US-0427982P.

PR

03-APR-2003; 2003US-0459782P.

XX

XX (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX

PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX

XX WPI; 2004-460799/43.

XX

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX

XX Disclosure; SEQ ID NO 4040; 350pp; English.

XX

XX The invention relate to a method of diagnosing (M1) non-blood disease

CC such as solid tumor by providing peripheral blood sample of human having

CC non-blood disease, and comparing an expression profile of specific genes

CC in the peripheral blood sample to reference expression profile of the

CC genes, where each of the genes is differentially expressed in peripheral

CC blood mononuclear cells (PBMCs) of patients having the disease as

CC compared to PBMCs of normal humans. The method is useful for diagnosing

CC non-blood disease such as solid tumor. The solid tumor is chosen from

CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The

CC peripheral blood sample comprises enriched PBMCs. The peripheral blood

CC sample is a whole blood sample (claimed). (M1) is useful for identifying

CC genes that are differentially expressed in peripheral blood samples

CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to

CC detect a gene that is differentially expressed and detected by the method  
XX of the invention.  
SQ Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 22 GCCACAGTCATGCCCGTCAG 3

RESULT 4  
ABN40468/c  
ID ABN40468 standard; DNA; 60 BP.  
XX  
AC ABN40468;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13216.

XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.

XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.

XX  
PR 28-JUL-2000; 2000US-0221607P.  
PR 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.

XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
DR

XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.

XX  
PS Example 1; SEQ ID NO 13216; 47pp; English.

XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 6 A; 18 C; 20 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 6.2; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 36 GCCACAGTCATGCCCGTCAG 17

RESULT 5  
ABA72432  
ID ABA72432 standard; DNA; 127 BP.

XX  
AC ABA72432;  
XX  
DT 01-FEB-2002 (first entry)

XX  
DE Human foetal liver single exon nucleic acid probe #20737.

XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX  
OS Homo sapiens.

XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.

XX  
PF 30-JAN-2001; 2001WO-US000669.

XX  
PR 04-FEB-2000; 2000US-0180312P.

XX  
PR 26-MAY-2000; 2000US-0207456P.

XX  
PR 30-JUN-2000; 2000US-00608408.

XX  
PR 03-AUG-2000; 2000US-00632366.

XX  
PR 21-SEP-2000; 2000US-0234687P.

XX  
PR 27-SEP-2000; 2000US-0236359P.

XX  
PR 04-OCT-2000; 2000GB-00024263.

XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX  
DR WPI; 2001-483447/52.

XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human foetal liver.

XX  
PS Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.

XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human foetal liver. The  
CC present sequence is a single exon nucleic acid probe of the invention.

CC  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 6

```

AAI52843
ID AAI52843 standard; DNA; 127 BP.
XX AC
XX AAI52843;
XX DT
XX 17-OCT-2001 (first entry)
XX DE
XX Probe #21529 used to measure gene expression in human placenta sample.
XX DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX KW
XX genetic disorder; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157272-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US0000663.
XX PR
XX 04-FEB-2000; 2000US-0180312P.
XX PR
XX 26-MAY-2000; 2000US-0207456P.
XX PR
XX 30-JUN-2000; 2000US-00608408.
XX PR
XX 03-AUG-2000; 2000US-00632366.
XX PR
XX 21-SEP-2000; 2000US-0234687P.
XX PR
XX 27-SEP-2000; 2000US-0236359P.
XX PR
XX 04-OCT-2000; 2000GB-00024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-488899/53.
XX PT
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT
XX hearts.
XX PS
XX Claim 4; SEQ ID NO 16681; 530pp; English.
XX CC
XX The present invention relates to single exon nucleic acid probes for
XX CC
XX measuring human gene expression in a sample derived from human heart. The
XX CC
XX present sequence is one such probe. The probes may be used for
XX CC
XX predicting, measuring and displaying gene expression in samples derived
XX CC
XX from the human heart via microarrays. By measuring gene expression, the
XX CC
XX probes are useful for predicting, diagnosing, grading, staging,
XX CC
XX monitoring and prognosing diseases of the human heart and vascular system
XX CC
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC
XX congenital heart disease. Note: The sequence data for this patent did not
XX CC
XX form part of the printed specification, but was obtained in electronic
XX CC
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
Db |||||
30 GCCACAGTCATGCCCGTCAG 49

RESULT 8
AAK47008
ID AAK47008 standard; DNA; 127 BP.
XX AC
XX AAK47008;
XX DT
XX 06-NOV-2001 (first entry)
XX DE
XX Human bone marrow expressed single exon probe SEQ ID NO: 21565.
XX XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157276-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US0000668.
XX PR
XX 04-FEB-2000; 2000US-0180312P.
XX PR
XX 26-MAY-2000; 2000US-0207456P.
XX PR
XX 30-JUN-2000; 2000US-00608408.
XX PR
XX 03-AUG-2000; 2000US-00632366.
XX PR
XX 21-SEP-2000; 2000US-0234687P.
XX PR
XX 27-SEP-2000; 2000US-0236359P.
XX PR
XX 04-OCT-2000; 2000GB-00024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-488899/53.
XX PT
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT
XX gene expression in human placenta.
XX PS
XX Claim 25; SEQ ID NO 21529; 654pp; English.
XX CC
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX CC
XX The present sequence is one such probe. The probes are useful for
XX CC
XX producing a microarray for predicting, measuring and displaying gene
XX CC
XX expression in samples derived from human placenta. The probes are useful
XX CC
XX for antenatal diagnosis of human genetic disorders
XX XX
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
Db |||||
30 GCCACAGTCATGCCCGTCAG 49

RESULT 7
ABA38215
ID ABA38215 standard; DNA; 127 BP.
XX AC
XX ABA38215;
XX DT
XX 23-JAN-2002 (first entry)
XX DE
XX Probe #16681 for gene expression analysis in human heart cell sample.
XX DE
XX Human; gene expression; heart; microarray; vascular system; probe;
XX KW
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW
XX congenital heart disease; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157274-A2.

```

```
PR 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCCACAGTCATGCCCGTCAG 20
Db 30 GCCACAGTCATGCCCGTCAG 49
RESULT 9
AAK20855
ID AAK20855 standard; DNA; 127 BP.
XX
AC AAK20855;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 20846.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple-sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
XX Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English.
XX
```

---

```
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system,
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCCACAGTCATGCCCGTCAG 20
Db 30 GCCACAGTCATGCCCGTCAG 49
RESULT 10
ABS46769
ID ABS46769 standard; DNA; 127 BP.
XX
AC ABS46769;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver single exon probe, SEQ ID NO 21759.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX coronary heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488998/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 21759; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
XX liver single exon nucleic acid probes of the invention. Note: The
XX sequence information for this patent does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
```

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 11
ABS21259
ID ABS21259 standard; DNA; 127 BP.
AC
XX
XX ABS21259;
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21250.
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US0000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 21250; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tubular sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
Db 30 GCCACAGTCATGCCCGTCAG 49

RESULT 12
ACH84269/c
ID ACH84269 standard; DNA; 179 BP.
XX
XX ACH84269;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #17464.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
```





KW ss; standardized polynucleotide system; medical diagnosis;  
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis.  
 OS Unidentified.  
 XX  
 PN DE10209071-A1.  
 XX  
 XX 25-SEP-2003.  
 XX  
 XX 28-FEB-2002; 2002DE-01009071.  
 PF  
 XX 28-FEB-2002; 2002DE-01009071.  
 PR  
 XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
 PA  
 XX Koehler T, Rost A;  
 PI  
 XX WPI; 2003-732912/70.  
 DR  
 XX  
 XX Standardized polynucleotide system, useful for quantitative, real-time  
 PT determination of nucleic acid, comprises stabilized standards, primers  
 PT and probe.  
 PT  
 XX  
 XX Claim 1; Page 7; 38pp; German.  
 PS  
 XX The present invention relates to a standardized polynucleotide system,  
 CC which comprises at least one carrier nucleic acid, at least 3  
 CC oligonucleotides, as primers and target-specific, fluorescently labeled  
 CC probe and optionally at least one set of stabilized controls (standard  
 CC RNA or DNA) of known concentration and instructions. The system comprises  
 CC any of 20 sets of one control, two primers and one target-specific probe.  
 CC The standardized polynucleotide system can be used for quantitative, real  
 CC -time detection of target nucleic acids, especially analysis of genes or  
 CC gene products, e.g. for individualized medical diagnosis, in veterinary  
 CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
 CC pharmaceutical testing, analysis of food or environmental samples and  
 CC also for ultra-sensitive detection of proteins by immuno-PCR. The present  
 CC sequence is a polynucleotide used in the system of the invention.  
 CC  
 SX Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 10; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCCACAGTCATGCCCGTCAG 20  
 Db 259 GCCACAGTCATGCCCGTCAG 240  
 RESULT 15  
 ACH46093/C  
 ID ACH46093 standard; cDNA; 492 BP.  
 AC ACH46093;  
 XX  
 XX 13-OCT-2003 (first entry)  
 DT  
 XX Human infant brain cDNA #156.  
 DE  
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX US2003073623-A1.  
 PN  
 XX 17-APR-2003.  
 PD  
 XX 30-JUL-2001; 2001US-00918995.  
 PF  
 XX 30-JUL-2001; 2001US-00918995.  
 PR  
 XX

PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX  
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX  
 XX WPI; 2003-615964/58.  
 DR  
 XX New polynucleotide sequences obtained from various cDNA libraries, useful  
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
 PT mapping, in the recombinant production of protein, or in generating  
 PT antisense DNA or RNA.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 33305; 44pp; English.  
 XX  
 XX The invention relates to an isolated polynucleotide comprising any one of  
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 CC determined by the technique of SBH (sequencing by hybridisation). Also  
 CC included is a purified polypeptide comprising a sequence corresponding to  
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 CC are useful in diagnostics as expressed sequence tags (EST) for  
 CC identifying expressed genes or for physical mapping of the human genome,  
 CC in forensics, in assessing biodiversity, or in identifying mutations,  
 CC responsible for genetic disorders and other traits. The nucleotide  
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 CC for chromosome and gene mapping, in the recombinant production of  
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 CC is useful for generating antibodies specific for it. The present sequence  
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
 CC  
 SX Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 9; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 7.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCCACAGTCATGCCCGTCAG 20  
 Db 443 GCCACAGTCATGCCCGTCAG 424  
 Search completed: February 4, 2005, 21:52:40  
 Job time : 261.033 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-3  
Perfect score: 20  
Sequence: 1 gccacagtcagccgcgtacg 20  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	119	2	BF840557 MR1-HT106
C 2	20	100.0	133	2	AW606507 MR2-HT038
C 3	20	100.0	140	2	BF948716 CM2-NN115
C 4	20	100.0	167	2	BF929309 IL2-NT020
C 5	20	100.0	177	9	CG642691 OST379295
C 6	20	100.0	194	2	BF80488 QV3-ET017
C 7	20	100.0	216	2	BF806802 PM2-CI011
C 8	20	100.0	227	9	CG656719 OST429779
C 9	20	100.0	233	1	AI904167 CM-BT043
C 10	20	100.0	253	9	CG659215 OST436826
C 11	20	100.0	254	7	T28063 EST26052 Hu
C 12	20	100.0	283	2	BF823588 RCS-RT005
C 13	20	100.0	332	2	AW820481 QV2-ST029
C 14	20	100.0	337	9	CG667740 OST461931
C 15	20	100.0	338	9	CG581705 OST222203
C 16	20	100.0	339	2	BE925384 PMO-AN008
C 17	20	100.0	356	2	AW244806 BR-END13C
C 18	20	100.0	374	9	CG524482 OST98550
C 19	20	100.0	374	9	CG631933 OST349236
C 20	20	100.0	391	9	CG624538 OST328585
C 21	20	100.0	396	4	BM818649 K-EST0085
C 22	20	100.0	403	9	CG632613 OST351228
C 23	20	100.0	412	9	CG559660 OST178957
C 24	20	100.0	413	9	CG663330 OST448394

C 25	20	100.0	415	9	CG531843
C 26	20	100.0	418	4	BI051278
C 27	20	100.0	418	4	BM741875
C 28	20	100.0	428	9	CG638384
C 29	20	100.0	442	1	AA903741
C 30	20	100.0	447	4	BM818387
C 31	20	100.0	466	9	CG592069
C 32	20	100.0	472	1	AI180733
C 33	20	100.0	475	5	BQ331598
C 34	20	100.0	482	2	BE378810
C 35	20	100.0	484	9	CG604974
C 36	20	100.0	486	9	CG598768
C 37	20	100.0	495	1	AA83283
C 38	20	100.0	496	7	CF725764
C 39	20	100.0	499	9	CG615667
C 40	20	100.0	501	4	BM090012
C 41	20	100.0	504	9	CG607848
C 42	20	100.0	508	9	CG607263
C 43	20	100.0	512	9	CG642256
C 44	20	100.0	512	9	CG646113
C 45	20	100.0	514	9	CG625069

## ALIGNMENTS

RESULT 1  
BF840557/c

LOCUS BF840557 119 bp mRNA linear EST 13-JAN-2001  
DEFINITION MR1-HT1067-011200-001-a10 HT1067 Homo sapiens cdna, mRNA sequence.

ACCESSION BF840557

VERSION BF840557.1 GI:12193055

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 119)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR1&t2=MR1-HT1067-

011200-001-a10&t3=2000-12-01&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 48

High quality sequence stop: 119.

Location/Qualifiers

1..119

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="HT1067"

/notes="Organ: head neck; Vector: puc18; Site:1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20  
|||||

Db 91 GCCACAGTCATGCCCGTCAG 72  
|||||

## RESULT 2

AW606507

LOCUS

MR2-HT0380-010200-101-f06 HT0380 Homo sapiens cDNA, mRNA sequence. EST 23-MAR-2000

ACCESSION

AW606507

VERSION

AW606507.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT0380-010200-101-f06&t3=2000-02-01&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 133.  
Location/Qualifiers  
1. 133  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HT0380"  
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## FEATURES

source

Query Match 100.0%; Score 20; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

QY 1 GCCACAGTCATGCCCGTCAG 20  
|||||

## Db

38 GCCACAGTCATGCCCGTCAG 57  
|||||

## RESULT 3

BF948716

LOCUS

IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 22-JAN-2001

## DEFINITION

ACCESSION

BF948716

VERSION

BF948716.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 31  
High quality sequence stop: 140.  
Location/Qualifiers  
1. 140  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NN1152"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## FEATURES

source

Query Match 100.0%; Score 20; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

QY 1 GCCACAGTCATGCCCGTCAG 20  
|||||

## Db

83 GCCACAGTCATGCCCGTCAG 102  
|||||

## RESULT 4

BF929309

LOCUS

IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

ACCESSION

BF929309

VERSION

BF929309.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

#### TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&tl2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 167.

Location/Qualifiers

1. .167

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="NT0202"

/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

#### FEATURES

source

1. .167

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="NT0202"

/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

#### ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

66 GCCACAGTCATGCCCGTCAG 85

#### RESULT 5

CG642691/c

LOCUS

DEFINITION

OST379295 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST379295, genomic survey sequence.

CG642691

CG642691.1 GI:37466540

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 177)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P.P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

#### TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

#### FEATURES

source

1. .194

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="ET0175"

/note="Organ: lung\_tumor; Vector: puc18; Site: 1: SmaI;

#### FEATURES

source

1. .177

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST379295"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

100 GCCACAGTCATGCCCGTCAG 81

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCCACAGTCATGCCCGTCAG 20

|||||

Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20  
|||||  
DB 125 GCCACAGTCATGCCCGTCAG 144

## RESULT 7

BF806802 216 bp mRNA linear EST 12-JAN-2001  
LOCUS PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BF806802  
ACCESSION BF806802.1 GI:12135791  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 216)  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jorgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

MEDLINE

PUBMED

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-091100-004-b10&t3=2000-11-09&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 25

High quality sequence stop: 216.

## FEATURES

source

1. 216  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CI0111"

/note="Organ: colon ins; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 50;

## Matches

20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GCCACAGTCATGCCCGTCAG 20

DB

65 GCCACAGTCATGCCCGTCAG 84

## RESULT 8

CG56719/c

LOCUS

DEFINITION

CG56719 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST429779, genomic survey sequence.

ACCESSION

CG56719

VERSION

CG56719.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 227)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, O., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmiBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene trap.

Location/Qualifiers

1. 227

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST429779"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 227;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GCCACAGTCATGCCCGTCAG 20

DB

87 GCCACAGTCATGCCCGTCAG 68

## RESULT 9

AI904167/c

LOCUS

DEFINITION

CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI904167

VERSION AI904167.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 233)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html>)  
&t3=090299&t4=1)

Seq primer: puc 18 forward.

Location/Qualifiers

1. .233  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="female"  
/dev stage="Adult"  
/clone lib="BT043"

/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

# ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 233;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

Db 96 GCCACAGTCATGCCCGTCAG 77

# RESULT 10

CG659215/c

LOCUS

DEFINITION OST436826 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST436826, genomic survey sequence.

ACCESSION

CG659215

VERSION

CG659215.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 253)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,

Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

# FEATURES

source

1. .253  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST436826"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

# ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 253;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACAGTCATGCCCGTCAG 20

Db 67 GCCACAGTCATGCCCGTCAG 48

# RESULT 11

T28063/c

LOCUS

DEFINITION

T28063

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 254)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,

Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,D.M., FitchHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S.,

Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,

Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,

Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,

Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,

Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,

Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,

Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,

Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,

Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,

Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,

Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

96026280

7566098

Other ESTs: THC20696

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .254

source

1. .254

source

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):101016"
/db_xref="taxon:9606"
/clone_lib="Human Brain"
/notes="Organ: brain"

ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 194 GCCACAGTCATGCCCGTCAG 175

RESULT 12
LOCUS BF823588 283 bp mRNA linear EST 13-JAN-2001
DEFINITION RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF823588
VERSION BF823588.1 GI:12164528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC5&t2=RC5-RT0055-
221200-011-G02&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 283.
FEATURES
source
1..283
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="RT0055"
/notes="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 263 GCCACAGTCATGCCCGTCAG 244

RESULT 14
LOCUS CG667740/c 337 bp DNA linear GSS 02-OCT-2003
DEFINITION OST461931 Mus musculus 129sv/Ev Mus musculus genomic clone
OST461931, genomic survey sequence.

```

```

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 111 GCCACAGTCATGCCCGTCAG 130

RESULT 13
LOCUS AW820481/c 332 bp mRNA linear EST 17-MAY-2000
DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW820481
VERSION AW820481.1 GI:7913475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 332)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV2=QV2-ST0298-140
200-042-f12&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
FEATURES
source
1..332
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0298"
/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGTCATGCCCGTCAG 20
    |||||
Db 263 GCCACAGTCATGCCCGTCAG 244

RESULT 14
LOCUS CG667740/c 337 bp DNA linear GSS 02-OCT-2003
DEFINITION OST461931 Mus musculus 129sv/Ev Mus musculus genomic clone
OST461931, genomic survey sequence.

```



```

ACCESSION   CG667740
VERSION     CG667740.1  GI:37491589
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
            Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
            Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
            Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
            Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
            Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
            Zhu, Q., Person, C. and Sands, A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES    source
            Location/Qualifiers
            1..337
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="129Sv/Ev"
            /db_xref="taxon:10090"
            /clones="OST222203"
            /cell_type="embryonic stem cell"
            /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 338;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCACAGTCATGCCCGTCAG 20
        |||||
Db      105 GCCACAGTCATGCCCGTCAG 86

Search completed: February 5, 2005, 08:11:31
Job time : 2390.67 secs

ACCESSION   CG667740
VERSION     CG667740.1  GI:37491589
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
            Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
            Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
            Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
            Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
            Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
            Zhu, Q., Person, C. and Sands, A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES    source
            Location/Qualifiers
            1..337
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="129Sv/Ev"
            /db_xref="taxon:10090"
            /clones="OST461931"
            /cell_type="embryonic stem cell"
            /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCACAGTCATGCCCGTCAG 20
        |||||
Db      86 GCCACAGTCATGCCCGTCAG 67

RESULT 15
CG581705/c
LOCUS       CG581705
DEFINITION OST222203 Mus musculus 129Sv/Ev Mus musculus genomic clone
            OST222203, genomic survey sequence.
ACCESSION   CG581705
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 338)
AUTHORS    Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
            Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
            Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
            Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
            Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
            Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
            Zhu, Q., Person, C. and Sands, A.T.
TITLE       Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES    source
            Location/Qualifiers
            1..338
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="129Sv/Ev"
            /db_xref="taxon:10090"
            /clones="OST222203"
            /cell_type="embryonic stem cell"
            /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 338;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCACAGTCATGCCCGTCAG 20
        |||||
Db      105 GCCACAGTCATGCCCGTCAG 86

Search completed: February 5, 2005, 08:11:31
Job time : 2390.67 secs

```

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-4  
Perfect score: 20  
Sequence: 1 ctgcgactccgactccaat 20  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235152
2	20	100.0	20	6	BD235167
3	20	100.0	555	6	CQ113695
4	20	100.0	555	6	CQ152574
5	20	100.0	555	6	CQ185831
6	20	100.0	555	6	CQ235904
7	20	100.0	555	6	CQ273477
8	20	100.0	555	6	CQ310858
9	20	100.0	555	6	CQ347773
10	20	100.0	600	6	CQ100639
11	20	100.0	600	6	CQ139631
12	20	100.0	600	6	CQ175964
13	20	100.0	600	6	CQ222999
14	20	100.0	600	6	CQ260961
15	20	100.0	600	6	CQ298444
16	20	100.0	600	6	CQ335104
17	20	100.0	636	6	BD097037
18	20	100.0	702	6	BD084108
19	20	100.0	702	6	BD102202

C 20	20	100.0	702	9	BT007208
C 21	20	100.0	702	12	BT008248
C 22	20	100.0	723	9	HSU072398
C 23	20	100.0	747	6	AX127722
C 24	20	100.0	926	6	AR054021
C 25	20	100.0	926	6	AR118504
C 26	20	100.0	926	6	AR124952
C 27	20	100.0	926	6	AR144311
C 28	20	100.0	926	6	AR172594
C 29	20	100.0	926	6	BD243042
C 30	20	100.0	926	6	CQ765842
C 31	20	100.0	926	6	E58777
C 32	20	100.0	926	6	I52011
C 33	20	100.0	926	6	AR371661
C 34	20	100.0	926	6	AR380885
C 35	20	100.0	926	6	AX839772
C 36	20	100.0	926	6	AX925686
C 37	20	100.0	926	9	HSBCLXL
C 38	20	100.0	1163	4	AB080951
C 39	20	100.0	1236	6	AX085490
C 40	20	100.0	1252	4	AB073983
C 41	20	100.0	1455	6	AX085496
C 42	20	100.0	2575	6	CQ827863
C 43	20	100.0	2575	9	EC019307
C 44	20	100.0	7372	6	E23357
C 45	20	100.0	81171	2	AC016218

ALIGNMENTS

RESULT 1  
LOCUS BD235152 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xl.  
ACCESSION BD235152  
VERSION BD235152.1 GI:33044922  
KEYWORDS JP 2002519048-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Stein,C.A.  
TITLE Oligonucleotide inhibitors of bcl-xl  
JOURNAL Patent: JP 2002519048-A 4 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/4  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PI 02-JUL-1998 US 09/109614  
CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Artificial Sequence'.  
FEATURES Location/Qualifiers  
source 1..20  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGCGATCCGACTCCAAT 20  
|||||

```

Db          1 CTGCGATCCGACTCACCACAT 20
RESULT 2
BD235167
LOCUS      BD235167
DEFINITION Oligonucleotide inhibitors of bcl-xL
ACCESSION  BD235167
VERSION     BD235167.1 GI:33044937
KEYWORDS   JP 2002519048-A/19
SOURCE     synthetic construct
ORGANISM   artificial sequences
REFERENCE  1 (bases 1 to 20)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 19 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/19
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PROPENYL dc
CC PROPENYL dt
CC PROPENYL dc
CC PROPENYL dt
CC PROPENYL dc
CC PROPENYL dt
CC PROPENYL dc
FH Key
FT misc_binding (2)..(3)
FT misc_binding (7)..(9)
FT misc_binding (12)..(14)
FT misc_binding (16)..(20)
FT modified_base (1)..(1)
FT modified_base (2)..(2)
FT modified_base (4)..(4)
FT modified_base (7)..(7)
FT modified_base (8)..(9)
FT modified_base (12)..(12)
FT modified_base (13)..(13)
FT modified_base (16)..(17)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 1 CTGCGATCCGACTCACCACAT 20
RESULT 3
CQ113695
LOCUS      CQ113695
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION  CQ113695
VERSION     CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
           Aeomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 63 CTGCGATCCGACTCACCACAT 82
RESULT 4
CQ152574
LOCUS      CQ152574
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION  CQ152574
VERSION     CQ152574.1 GI:41159924
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human bone marrow
JOURNAL    Patent: WO 0157276-A 22596 09-AUG-2001;
           Aeomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 63 CTGCGATCCGACTCACCACAT 82
RESULT 5
CQ185831
LOCUS      CQ185831
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION  CQ113695
VERSION     CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
           Aeomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCGATCCGACTCACCACAT 20
|||||
Db 63 CTGCGATCCGACTCACCACAT 82

```

LOCUS  
 DEFINITION Sequence 17227 from Patent WO0157274.  
 ACCESSION CQ185831  
 VERSION CQ185831.1 GI:41180846  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1  
 REFERENCE Penn.S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
 AUTHORS Human genome-derived single exon nucleic acid probes useful for  
 TITLE analysis of gene expression in human heart  
 JOURNAL Patent: WO 0157274-A 17227 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..555  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =  
 1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
 BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
 0.00e+00"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTGCGATCCGACTCACCACAT 20  
 ||||||||||||||||||  
 Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 6  
 LOCUS CQ235904  
 DEFINITION Sequence 22743 from Patent WO0157273.  
 ACCESSION CQ235904  
 VERSION CQ235904.1 GI:41219182  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1  
 REFERENCE Penn.S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
 AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 TITLE ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
 (03.10.00)<150> US 60/236,359<151> 27 September 2000  
 (27.09.00)<150> US 60/234,687<151> 21 September 2000  
 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
 Molecular Dynamics Sequence Listing Engine  
 Patent: WO 0157273-A 22743 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..555  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL  
 = 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN  
 HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
 0.00e+00"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20  
 ||||||||||||||||||  
 Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 7  
 LOCUS CQ273477  
 DEFINITION Sequence 21738 from Patent WO0157277.  
 ACCESSION CQ273477  
 VERSION CQ273477.1 GI:41246081  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1  
 REFERENCE Penn.S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
 AUTHORS Human genome-derived single exon nucleic acid probes useful for  
 TITLE analysis of gene expression in human fetal liver  
 JOURNAL Patent: WO 0157277-A 21738 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..555  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL  
 = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN  
 HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
 0.00e+00"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTGCGATCCGACTCACCACAT 20  
 ||||||||||||||||||  
 Db 63 CTGCGATCCGACTCACCACAT 82

RESULT 8  
 LOCUS CQ310858  
 DEFINITION Sequence 21963 from Patent WO0186003.  
 ACCESSION CQ310858  
 VERSION CQ310858.1 GI:41271435  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1  
 REFERENCE Penn.S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
 AUTHORS Human genome-derived single exon nucleic acid probes useful for  
 TITLE analysis of gene expression in human lung  
 JOURNAL Patent: WO 0186003-A 21963 15-NOV-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..555  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =  
 2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
 BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
 0.00e+00"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 8.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 9  
 CQ347773  
 LOCUS 555 bp DNA linear PAT 23-JAN-2004  
 DEFINITION Sequence 21867 from Patent WO0157275.  
 ACCESSION CQ347773  
 VERSION CQ347773.1 GI:41296844  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human brain  
 JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;  
 Aeomica, Inc. (US)

FEATURES  
 source  
 1..555  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =  
 1.6-SWISSPROT HIT: Q07817, EVALU 1.00e-106-BST HUMAN HIT:  
 BE207063.1, EVALU 0.00e+00-NT HIT: U72398.1, EVALU  
 0.00e+00"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 10  
 CQ100639  
 LOCUS 600 bp DNA linear PAT 21-JAN-2004  
 DEFINITION Sequence 9498 from Patent WO0157272.  
 ACCESSION CQ100639  
 VERSION CQ100639.1 GI:41069665  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human placenta  
 JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;  
 Aeomica, Inc. (US)

FEATURES  
 source  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =  
 0.99"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 82 CTGCGATCCGACTCACC AAT 101

RESULT 11  
 CQ139631  
 LOCUS 600 bp DNA linear PAT 21-JAN-2004  
 DEFINITION Sequence 9653 from Patent WO0157276.  
 ACCESSION CQ139631  
 VERSION CQ139631.1 GI:41097003  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human bone marrow  
 JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;  
 Aeomica, Inc. (US)

FEATURES  
 Location/Qualifiers  
 source  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL  
 = 4.7"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 82 CTGCGATCCGACTCACC AAT 101

RESULT 12  
 CQ175964  
 LOCUS 600 bp DNA linear PAT 21-JAN-2004  
 DEFINITION Sequence 7360 from Patent WO0157274.  
 ACCESSION CQ175964  
 VERSION CQ175964.1 GI:41170703  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human heart  
 JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;  
 Aeomica, Inc. (US)

FEATURES  
 Location/Qualifiers  
 source  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 82 CTGCGATCCGACTCACC AAT 101

```

RESULT 13
CQ222999
LOCUS      CQ222999
DEFINITION Sequence 9838 from Patent WO0157273.
ACCESSION CQ222999
VERSION    CQ222999.1 GI:41205280
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
            3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
            60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
            August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
            (03.10.00)<150> US 60/236,359<151> 27 September 2000
            (27.09.00)<150> US 60/234,687<151> 21 September 2000
            (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
            Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 9838 09-AUG-2001;
            Acomica, Inc. (US)
FEATURES     source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
            = 1.7"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

RESULT 14
CQ260961
LOCUS      CQ260961
DEFINITION Sequence 9222 from Patent WO0157277.
ACCESSION CQ260961
VERSION    CQ260961.1 GI:41233441
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
JOURNAL      Patent: WO 0157277-A 9222 09-AUG-2001;
            Acomica, Inc. (US)
FEATURES     source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
            = 3.5"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

RESULT 15
CQ298444
LOCUS      CQ298444
DEFINITION Sequence 9549 from Patent WO0186003.
ACCESSION CQ298444
VERSION    CQ298444.1 GI:41259021
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
JOURNAL      Patent: WO 0186003-A 9549 15-NOV-2001;
            Acomica, Inc. (US)
FEATURES     source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGATCCGACTCACCACAT 20
        |||||
Db      82 CTGGATCCGACTCACCACAT 101

Search completed: February 4, 2005, 23:30:40
Job time : 482.738 secs

```

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169a-4

Perfect score: 20

Sequence: 1 ctgcgatccgactcaccacat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	AZ46974 Bcl-X1 MR
2	20	100.0	25	10	ADK66040 Standard
3	20	100.0	337	10	ADK66037 Standard
4	20	100.0	492	9	ACH46093 Human inf
5	20	100.0	555	4	ABA73433 Human foe
6	20	100.0	555	4	AAI53868 Probe #22
7	20	100.0	555	4	ABA38761
8	20	100.0	555	4	AAK48039
9	20	100.0	555	4	AAK21876
10	20	100.0	555	4	ABS47753
11	20	100.0	555	6	ABS21972
12	20	100.0	564	12	ACH87595
13	20	100.0	600	4	ABA60917
14	20	100.0	600	4	AAI40812
15	20	100.0	600	4	ABA28894
16	20	100.0	600	4	AAK35096
17	20	100.0	600	4	AAK09207
18	20	100.0	600	4	ABS34848
19	20	100.0	600	6	ABS09558
20	20	100.0	636	4	AAH48169
21	20	100.0	702	5	AAH43464

#### ALIGNMENTS

RESULT 1

AZ46974

ID AZ46974 standard; DNA; 20 BP.

XX

AC AZ46974;

XX

DT 14-APR-2000 (first entry)

XX

DE Bcl-X1 mRNA specific antisense oligo D.

XX

KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;

KW lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX

OS Homo sapiens.

XX

PN WO200001393-A2.

XX

PD 13-JAN-2000.

XX

PF 02-JUL-1999; 99WO-US015250.

XX

PR 02-JUL-1998; 98US-00109614.

XX

PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Stein CA;

XX

DR WPI; 2000-137140/12.

XX

PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX

PS Claim 1; Fig 1; 69pp; English.

XX

CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX  
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 DB 1 CTGCGATCCGACTCACCACAT 20

RESULT 2  
 ADK66040/c  
 ID ADK66040 standard; DNA; 25 BP.  
 XX  
 AC ADK66040;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Standardized polynucleotide system polynucleotide #8 probe.  
 XX  
 KW ss; standardized polynucleotide system; medical diagnosis;  
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis;  
 KW probe.  
 XX  
 OS Unidentified.  
 XX  
 PN DE10209071-A1.  
 XX  
 PD 25-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01009071.  
 XX  
 PR 28-FEB-2002; 2002DE-01009071.  
 XX

XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
 XX Koehler T, Rost A;  
 XX WPI; 2003-732912/70.  
 XX  
 XX Standardized polynucleotide system, useful for quantitative, real-time  
 XX determination of nucleic acid, comprises stabilized standards, primers  
 XX and probe.  
 XX  
 PS Claim 1; Page 7; 38pp; German.  
 XX  
 XX The present invention relates to a standardized polynucleotide system,  
 XX which comprises at least one carrier nucleic acid, at least 3  
 XX oligonucleotides, as primers and target-specific, fluorescently labeled  
 XX probe and optionally at least one set of stabilized controls (standard  
 XX RNA or DNA) of known concentration and instructions. The system comprises  
 XX any of 20 sets of one control, two primers and one target-specific probe.  
 XX The standardized polynucleotide system can be used for quantitative, real  
 XX -time detection of target nucleic acids, especially analysis of genes or  
 XX gene products, e.g. for individualized medical diagnosis, in veterinary  
 XX medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
 XX pharmaceutical testing, analysis of food or environmental samples and  
 XX also for ultra-sensitive detection of proteins by immuno-PCR. The present  
 XX sequence is a probe used to isolate a polynucleotide used in the system  
 XX of the invention.

XX  
 SQ Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 DB 20 CTGCGATCCGACTCACCACAT 1

RESULT 3  
 ADK66037/c  
 ID ADK66037 standard; DNA; 337 BP.  
 XX  
 AC ADK66037;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Standardized polynucleotide system polynucleotide #8.  
 XX  
 KW ss; standardized polynucleotide system; medical diagnosis;  
 KW functional genomics; sample analysis; pharmacogenomics; sample analysis.  
 KW Unidentified.  
 XX  
 PN DE10209071-A1.  
 XX  
 PD 25-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01009071.  
 XX  
 PR 28-FEB-2002; 2002DE-01009071.  
 XX

XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
 XX Koehler T, Rost A;  
 XX WPI; 2003-732912/70.  
 XX  
 XX Standardized polynucleotide system, useful for quantitative, real-time  
 XX determination of nucleic acid, comprises stabilized standards, primers  
 XX and probe.  
 XX  
 PS Claim 1; Page 7; 38pp; German.  
 XX  
 XX The present invention relates to a standardized polynucleotide system,  
 XX which comprises at least one carrier nucleic acid, at least 3  
 XX oligonucleotides, as primers and target-specific, fluorescently labeled  
 XX probe and optionally at least one set of stabilized controls (standard  
 XX RNA or DNA) of known concentration and instructions. The system comprises  
 XX any of 20 sets of one control, two primers and one target-specific probe.  
 XX The standardized polynucleotide system can be used for quantitative, real  
 XX -time detection of target nucleic acids, especially analysis of genes or  
 XX gene products, e.g. for individualized medical diagnosis, in veterinary  
 XX medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
 XX pharmaceutical testing, analysis of food or environmental samples and  
 XX also for ultra-sensitive detection of proteins by immuno-PCR. The present  
 XX sequence is a polynucleotide used in the system of the invention.

XX  
 SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 DB 99 CTGCGATCCGACTCACCACAT 80

RESULT 4  
 ACH46093/c  
 ID ACH46093 standard; cDNA; 492 BP.  
 XX  
 AC ACH46093;  
 XX  
 DT 13-OCT-2003 (first entry)  
 XX

```

DE Human infant brain cDNA #156.
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
OS US2003073623-A1.
PN 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.
PA (DICK//) DICKSON M C.
PA (JONE//) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX Claim 1; SEQ ID NO 33305; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGATCCGACTCACCACAT 20
DB 283 CTGGGATCCGACTCACCACAT 264
RESULT 5
ABA73433
ID ABA73433 standard; DNA; 555 BP.
XX
XX ABA73433;
AC ABA73433;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #21738.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX

```

---

```

OS Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US0000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGATCCGACTCACCACAT 20
DB 63 CTGGGATCCGACTCACCACAT 82
RESULT 6
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX
XX AAI53868;
AC AAI53868;
XX
XX 17-OCT-2001 (first entry)
XX
XX Probe #22554 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US0000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.

```

```
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
DR WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX Claim 25; SEQ ID NO 22554; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 7
ABA38761
ID ABA38761 standard; DNA; 555 BP.
XX AC ABA38761;
XX 23-JAN-2002 (first entry)
XX DE Probe #1727 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX Claim 4; SEQ ID NO 17227; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACC AAT 20
Db 63 CTGCGATCCGACTCACC AAT 82

RESULT 8
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX AC AAK48039;
XX 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6;
```

DT	25-FEB-2003	(first entry)
XX	Human liver single exon probe, SEQ ID No 22743.	
XX	Human; single exon nucleic acid probe; liver; cirrhosis;	
XX	hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;	
KW	coronary heart disease; ss.	
XX	Homo sapiens.	
OS	WO200157273-A2.	
PN	09-AUG-2001.	
XX	XX	
PF	30-JAN-2001; 2001WO-US000664.	
XX	04-FEB-2000; 2000US-0180312P.	
PR	26-MAY-2000; 2000US-0207456P.	
PR	30-JUN-2000; 2000US-00608408.	
PR	03-AUG-2000; 2000US-00632366.	
PR	21-SEP-2000; 2000US-0234687P.	
PR	27-SEP-2000; 2000US-0236359P.	
PR	04-OCT-2000; 2000GB-00024263.	
XX	(MOLE-) MOLECULAR DYNAMICS INC.	
FA	Penn SG, Hanzel DK, Chen W, Rank DR;	
PI	WPI; 2001-488898/53.	
XX	Human genome-derived single exon nucleic acid probes useful for analyzing	
PT	gene expression in human adult liver.	
PS	Claim 4; SEQ ID NO 22743; 658pp; English.	
XX	The invention relates to a single exon nucleic acid probe (SENP) (I) for	
CC	measuring human gene expression in a sample derived from human adult	
CC	liver, comprising one of 13109 defined nucleotide sequences given in the	
CC	specification (or complements/ fragments). The probe hybridises at high	
CC	stringency to a nucleic acid molecule expressed in the human adult liver.	
CC	(I) may be used for predicting, measuring and displaying gene expression	
CC	in samples derived from human adult liver. The genes identified may be	
CC	involved in genetic liver diseases such as cirrhosis,	
CC	hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is	
CC	associated with coronary heart disease. ABS25011-ABS51005 represent human	
CC	liver single exon nucleic acid probes of the invention. Note: The	
CC	sequence information for this patent does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 555 BP; 105 A; 178 G; 133 T; 0 U; 0 Other;	
QY	Query Match 100.0%; Score 20; DB 4; Length 555;	
DB	Best Local Similarity 100.0%; Pred. No. 1.6;	
DB	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CTGGATCCGACTCACCACAT 20	
DB	63 CTGGATCCGACTCACCACAT 82	
RESULT 11		
ABS21972		
ID	ABS21972 standard; DNA; 555 BP.	
XX	XX	
AC	ABS21972;	
XX	XX	
DT	19-AUG-2002 (first entry)	
XX	Human genome-derived single exon probe ORF from lung SEQ ID No 21963.	
XX	Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;	
KW	chronic obstructive pulmonary disease; interstitial lung disease;	

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagazer syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease; open reading frame; ORF.  
XX  
OS Homo sapiens.  
XX  
PN WO200186003-A2.  
XX  
PD 15-NOV-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000665.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.  
XX  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples.  
XX  
XX Claim 4; SEQ ID NO 21963; 634pp; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of probes  
CC; the novel set of probes which hybridise at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGGGATCCGACTCACCACAT 20  
DB 63 CTGGGATCCGACTCACCACAT 82  
RESULT 12  
ACH87595  
ID ACH87595 standard; DNA; 564 BP.  
XX  
AC ACH87595;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon probe #20790.  
XX  
KW Human; probe; ss; gene expression; single exon probe; microarray;  
KW alternative splicing event; genomic alteration.  
XX  
OS Homo sapiens.  
XX  
XX US2003194704-A1.  
XX  
PD 16-OCT-2003.  
XX  
XX 03-APR-2002; 2002US-00029386.  
XX  
XX 03-APR-2002; 2002US-00029386.  
XX  
XX (PENN/) PENN S G.  
XX PA (RANK/) RANK D R.  
XX PA (HANZ/) HANZEL D K.  
XX  
XX Penn SG, Rank DR, Hanzel DK;  
XX WPI; 2004-119264/12.  
XX  
XX New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
XX Claim 1; SEQ ID NO 20790; 80pp; English.  
XX  
XX The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and  
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
CC fully defined in the specification. The probe is a single exon probe that  
CC hybridises under high stringency conditions to a nucleic acid molecule  
CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterizing  
 CC alternative splicing events, in detecting and characterizing gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids, or  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTCACCACAT 20  
 Db 63 CTGGATCCGACTCACCACAT 82

#### RESULT 13

ID ABA60917 standard; DNA; 600 BP.

AC ABA60917;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #9222.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

XX WO200157277-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US0000669.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

PS Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTCACCACAT 20  
 Db 82 CTGGATCCGACTCACCACAT 101

#### RESULT 14

ID AAI40812 standard; DNA; 600 BP.

XX AAI40812;

DT 17-OCT-2001 (first entry)

DE Probe #9498 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder; ss.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 9498; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGATCCGACTCACCACAT 20

Db 82 CTGGATCCGACTCACCACAT 101

RESULT 15

ABA28894

ID ABA28894 standard; DNA; 600 BP.

XX ABA28894;

XX AC

XX XX

DT 23-JAN-2002 (first entry)  
XX  
DE Probe #7360 for gene expression analysis in human heart cell sample.  
XX  
XX Human; gene expression; heart; microarray; vascular system; probe;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
XX  
PD 09-AUG-2001.  
XX  
XX  
PF 30-JAN-2001; 2001WO-US000666.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234887P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GE-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488899/53.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX  
PS Claim 1; SEQ ID NO 7360; 530pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGCGATCCGACTCACCAT 20  
DB 82 CTGCGATCCGACTCACCAT 101

Search completed: February 4, 2005, 21:52:41  
Job time : 259.033 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-4

Perfect score: 20

Sequence: 1 ctgcgatccactccaacat 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	167	4	BM820203
C 2	20	100.0	332	2	AW820481
C 3	20	100.0	396	4	BM818649
C 4	20	100.0	418	4	BT051278
C 5	20	100.0	437	7	W01420
C 6	20	100.0	447	4	BM818387
C 7	20	100.0	456	8	AZ537061
C 8	20	100.0	478	4	BM050133
C 9	20	100.0	485	2	AW814883
C 10	20	100.0	555	2	BE393580
C 11	20	100.0	563	2	BE617040
C 12	20	100.0	579	4	BM741157
C 13	20	100.0	620	4	BM820164
C 14	20	100.0	657	2	BE207063
C 15	20	100.0	681	6	CF147016
C 16	20	100.0	687	2	BE293685
C 17	20	100.0	695	4	BE125492
C 18	20	100.0	697	4	BE457116
C 19	20	100.0	699	2	BE870269
C 20	20	100.0	700	4	BE831301
C 21	20	100.0	705	4	BE290422
C 22	20	100.0	711	2	BE535474
C 23	20	100.0	714	4	BE470667
C 24	20	100.0	798	5	BU528551

C 25	20	100.0	798	7	CK000319
C 26	20	100.0	808	4	BI222971
C 27	20	100.0	818	4	BG824757
C 28	20	100.0	830	7	CF619432
C 29	20	100.0	836	4	BM018295
C 30	20	100.0	843	5	BQ962018
C 31	20	100.0	845	5	BU527940
C 32	20	100.0	859	6	CD359906
C 33	20	100.0	860	1	AL537680
C 34	20	100.0	872	5	BU168531
C 35	20	100.0	874	5	BU844419
C 36	20	100.0	878	5	BQ888053
C 37	20	100.0	882	5	BQ646768
C 38	20	100.0	901	5	BQ940282
C 39	20	100.0	912	5	BQ935725
C 40	20	100.0	919	5	BQ948029
C 41	20	100.0	920	5	BQ646527
C 42	20	100.0	920	5	BU528504
C 43	20	100.0	922	5	BQ924197
C 44	20	100.0	923	5	BQ927754
C 45	20	100.0	925	4	BM018845

## ALIGNMENTS

### RESULT 1

BM820203/c

LOCUS

DEFINITION

K-EST0088575 S20T665307 Homo sapiens cDNA clone S20T665307-9-G04

167 bp mRNA linear EST 06-MAR-2002

S., mRNA sequence.

ACCESSION

BM820203

VERSION

BM820203.1 GI:19176616

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 167)

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 9 row: G column: 04

High quality sequence stop: 167.

Location/Qualifiers

1. 167

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S20T665307-9-G04"

/sex="M"

/lab\_host="Top10F"

/clone\_lib="S20T665307"

/notes="Organ: Stomach; Vector: pCNS; Site 1: EcorI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated with

with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including Ecor

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcorI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;  
 QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 Db 136 CTGCGATCCGACTCACCACAT 117

## RESULT 2

AW820481/c  
 LOCUS  
 DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW820481  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)

## REFERENCE

AUTHORS  
 1 (bases 1 to 332)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, D.F., de Souza, S.J. and Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## JOURNAL

MEDLINE  
 PUBMED  
 COMMENT  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=at2=QV2-ST0298-140200-042-f12&t3=2000-02-14&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 332.

## FEATURES

## source

1..332  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="ST0298"  
 /note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 7.7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 Db 103 CTGCGATCCGACTCACCACAT 84

## RESULT 3

BM818649/c  
 LOCUS  
 DEFINITION K-EST0085991 S20T665307 Homo sapiens CDNA clone S20T665307-4-F03 5', mRNA sequence.  
 ACCESSION BM818649  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)

## REFERENCE

AUTHORS  
 1 (bases 1 to 396)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ann, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

## TITLE

21C Frontier Korean EST Project 2001

## JOURNAL

## COMMENT

Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 4 row: F column: 03  
 High quality sequence stop: 396.

## FEATURES

## source

1..396  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S20T665307-4-F03"  
 /sex="M"  
 /lab\_host="Top10F"  
 /clone\_lib="S20T665307"  
 /note="Organ: Stomach; Vector: pcns; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including BcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 7.8; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;

QY 1 CTGCGATCCGACTCACCACAT 20  
 |||||  
 Db 136 CTGCGATCCGACTCACCACAT 117

## RESULT 4

BI051278  
 LOCUS  
 DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BI051278

```

VERSION      BI051278.1  GI:14459808
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 418)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Ngai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&tl2=CM3-GN0297-
              110101-607-f03&tl3=2001-01-11&tl4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 3
              High quality sequence stop: 418.
              Location/Qualifiers
FEATURES     source
              1..418
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="GN0297"
                /note="Organ: placenta normal; Vector: puc18; Site 1:
                SmaI; Site 2: SmaI; A mini-library was made by cloning
                products derived from ORESTES PCR (U.S. Letters Patent
                application No. 196,716 - Ludwig Institute for Cancer
                Research) profiles into the pUC 18 vector. Reverse
                transcription of tissue mRNA and cDNA amplification were
                performed under low stringency conditions."
ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGATCCGACTCACCACAT 20
    |||||
Db 223 CTGGGATCCGACTCACCACAT 242

RESULT 5
LOCUS      W01420
DEFINITION W01420.1 Soares fetal lung NbHL19W Homo sapiens cDNA clone
            IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
            BCL-X., mRNA sequence.
ACCESSION  W01420
VERSION     W01420.1  GI:1273428
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 437)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasaki,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@wustl.edu
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: mob.REGA+ET
              High quality sequence stop: 383.
              Location/Qualifiers
FEATURES     source
              1..437
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:1243109"
                /db_xref="taxon:9606"
                /clone="IMAGE:298187"
                /dev_stage="19 weeks"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares fetal lung NbHL19W"
                /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer
                [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTT-3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT7T3 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by Bento
                Soares and M.Fatima Bonaldo. This library was constructed
                from the same fetus as the fetal heart library. Soares
                fetal heart NbHL19W."
ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 437;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGATCCGACTCACCACAT 20
    |||||
Db 258 CTGGGATCCGACTCACCACAT 239

RESULT 6
LOCUS      BM818387/c
DEFINITION K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
            5', mRNA sequence.
ACCESSION  BM818387
VERSION     BM818387.1  GI:19174800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 447)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            21C Frontier Korean EST Project 2001
            Unpublished (2002)
            Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409

```

Email: yongsung@mail.kribb.re.kr  
Plate: 3 Row: B column: 02  
High quality sequence stop: 447.

# FEATURES

Location/Qualifiers  
1. .447  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S20T665307-3-B02"  
/sex="M"  
/lab\_host="Top10F"  
/clone\_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 447;  
Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0

QY 1 CTGCGATCCGACTCACCACAT 20  
|||||  
DB 136 CTGCGATCCGACTCACCACAT 117

## RESULT 7

AZ537061  
LOCUS AST-2P01514, AB Genetrapp PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.  
DEFINITION

ACCESSION AZ537061  
VERSION AZ537061.1 GI:11113828  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M., Bernardino, A., Durick, K. and Pollok, B.

## REFERENCE

AUTHORS Exon-trap tags from a PC-3 GenomeScreen(TM) Library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Greg Henkel  
Gene Expression  
Aurora Biosciences Corp.  
11010 Torreyana Road, San Diego, CA 92121, USA  
Tel: 8584048436  
Fax: 8584046719

## FEATURES

Location/Qualifiers  
1. .456  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/tissue\_type="Adenocarcinoma"  
/cell\_type="Epithelial"  
/clone\_lib="Genetrapp PC-3 Human Prostatic Carcinoma Library"

/note="Organ: prostate; Vector: pAMP-1; 3' RACE of total RNA from genetrapp pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."  
Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 478;

## Class: exon-trapped.

### Location/Qualifiers

1. .456  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/tissue\_type="Adenocarcinoma"  
/cell\_type="Epithelial"  
/clone\_lib="Genetrapp PC-3 Human Prostatic Carcinoma Library"

/note="Organ: prostate; Vector: pAMP-1; 3' RACE of total RNA from genetrapp pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

## ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0

QY 1 CTGCGATCCGACTCACCACAT 20  
|||||  
DB 194 CTGCGATCCGACTCACCACAT 213

## RESULT 8

### BM050133/c

LOCUS 603632480F1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5422338 5', mRNA sequence.  
DEFINITION

ACCESSION BM050133  
VERSION BM050133.1 GI:16779400  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 478)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC

## REFERENCE

AUTHORS cDNA Library Preparation: Ling Hong/Rubin Laboratory  
TITLE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
JOURNAL DNA Sequencing by: Incyte Genomics, Inc.  
COMMENT Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM1879 row: p column: 19  
High quality sequence stop: 267.  
Location/Qualifiers  
1. .478  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5422338"  
/tissue\_type="epithelioid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_42"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"

## FEATURES

Location/Qualifiers  
1. .478  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5422338"  
/tissue\_type="epithelioid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_42"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"

Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACCACAT 20  
Db 242 CTGCGATCCGACTCACCACAT 223

## RESULT 9

AW814883

## LOCUS

DEFINITION MR1-ST0206-120400-022-f04 ST0206 Homo sapiens CDNA, mRNA linear EST 17-MAY-2000

## ACCESSION

AW814883

## VERSION

AW814883.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 486)

## AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

## JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## MEDLINE

20202663

## PUBMED

10737800

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-mr1-ST0206-120400-022-f04&amp;t3=2000-04-12&amp;t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

## FEATURES

Location/Qualifiers

1..486

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev stage="Adult"

/clone\_lib="ST0206"

/note="Organ: stomach; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 7.9; Mismatches 0; Indels 0; Gaps 0;

## Qy

1 CTGCGATCCGACTCACCACAT 20

## Db

185 CTGCGATCCGACTCACCACAT 204

## RESULT 10

BE393580/c

## LOCUS

DEFINITION

601310279F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3632058 5', mRNA sequence.

## ACCESSION

BE393580

## VERSION

BE393580.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 555)

## AUTHORS

NTH-MGC http://mgc.nci.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LCM322 row: m column: 19

High quality sequence stop: 551.

## FEATURES

Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:3632058"

/tissue\_type="endometrium, adenocarcinoma cell line"

/lab host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 44"

/note="Organ: uterus; Vector: pCM87; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 8; Mismatches 0; Indels 0; Gaps 0;

## Qy

1 CTGCGATCCGACTCACCACAT 20

## Db

71 CTGCGATCCGACTCACCACAT 52

## RESULT 11

BE617040/c

## LOCUS

DEFINITION

601441454F1 NIH\_MGC\_65 Homo sapiens CDNA clone IMAGE:3845892 5', mRNA sequence.

## ACCESSION

BE617040

## VERSION

BE617040.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 563)

## AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLAM9557 row: k column: 13  
 High quality sequence stop: 561.

## FEATURES

Location/Qualifiers

1..563  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3845892"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="NIH\_MGC\_65"  
 /clone\_lib="NIH\_MGC\_65"  
 /note="Organ: colon; Vector: pCMV-SpOrt6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.8 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20

Db 37 CTGCGATCCGACTCACCACAT 18

## RESULT 12

BM741157/c

LOCUS BM741157 579 bp mRNA linear EST 01-MAR-2002  
 DEFINITION K-EST0013545 S6SNU620 Homo sapiens cDNA clone S6SNU620-6-A10 5',  
 mRNA sequence.

ACCESSION BM741157.1 GI:19062486

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 579)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT

Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 6 row: A column: 10

High quality sequence stop: 579.

## FEATURES

source

Location/Qualifiers

1..579  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S6SNU620-6-A10"  
 /sex="F"  
 /tissue\_type="Ascites"  
 /cell\_type="Scattering floating"  
 /cell\_line="SNU-620"  
 /lab\_host="Top10F"  
 /clone\_lib="S6SNU620"  
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 579;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCGATCCGACTCACCACAT 20

Db 164 CTGCGATCCGACTCACCACAT 145

## RESULT 13

BM820164/c

LOCUS BM820164 620 bp mRNA linear EST 06-MAR-2002  
 DEFINITION K-EST0089533 S20T65307 Homo sapiens cDNA clone S20T65307-9-C10  
 5', mRNA sequence.

ACCESSION BM820164

VERSION BM820164.1 GI:19176577

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 620)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 9 row: C column: 10

High quality sequence stop: 620.

## FEATURES

source

Location/Qualifiers

1..620  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S20T65307-9-C10"  
 /sex="M"  
 /lab\_host="Top10F"  
 /clone\_lib="S20T65307"  
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 136 CTGCGATCCGACTCACC AAT 117

RESULT 14  
 BE207063/c  
 LOCUS

DEFINITION  
 ba09f05.y1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:2823873 5', similar to cb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);, mRNA sequence.

ACCESSION  
 BE207063  
 VERSION  
 BE207063.1 GI:8750461  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 1 (bases 1 to 657)  
 AUTHORS  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Other ESTs: ba09f05.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 450.

FEATURES  
 source  
 1..657  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2823873"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 657;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 533 CTGCGATCCGACTCACC AAT 514

RESULT 15  
 CF147016/c  
 LOCUS

DEFINITION  
 UI-HF-CB0-atf-g-11-0-UI.r1 NIH MGC 210 Homo sapiens cDNA clone IMAGE:30570802 5', mRNA sequence.

ACCESSION  
 CF147016  
 VERSION  
 CF147016.1 GI:33262460  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 1 (bases 1 to 681)  
 AUTHORS  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE  
 Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Tim Ratliff  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html  
 Seq primer: pYX-5.

FEATURES  
 Location/Qualifiers  
 1..681  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30570802"  
 /tissue\_type="CNCAP(3)T-225 cell line"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH MGC 210"  
 /note="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR 1; Site 2: Not 1; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dt primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 681;  
 Best Local Similarity 100.0%; Pred. No. 8.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGATCCGACTCACC AAT 20  
 |||||  
 Db 38 CTGCGATCCGACTCACC AAT 19

Search completed: February 5, 2005, 08:11:37  
 Job time : 2390.67 secs

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-5  
Perfect score: 18  
Sequence: 1 agtcctgttcttccac 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644845745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hhg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_rts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	6	BD235153	BD235153 Oligonucleotide inhibitors of bcl-xL
2	18	100.0	18	6	BD235168	BD235168 Oligonucleotide inhibitors of bcl-xL
3	18	100.0	512	6	CQ727769	CQ727769 Sequence
4	18	100.0	555	6	CQ113695	CQ113695 Sequence
5	18	100.0	555	6	CQ152574	CQ152574 Sequence
6	18	100.0	555	6	CQ185831	CQ185831 Sequence
7	18	100.0	555	6	CQ235904	CQ235904 Sequence
8	18	100.0	555	6	CQ273477	CQ273477 Sequence
9	18	100.0	555	6	CQ310858	CQ310858 Sequence
10	18	100.0	555	6	CQ347773	CQ347773 Sequence
11	18	100.0	600	6	CQ106639	CQ106639 Sequence
12	18	100.0	600	6	CQ139631	CQ139631 Sequence
13	18	100.0	600	6	CQ175964	CQ175964 Sequence
14	18	100.0	600	6	CQ222999	CQ222999 Sequence
15	18	100.0	600	6	CQ260961	CQ260961 Sequence
16	18	100.0	600	6	CQ298444	CQ298444 Sequence
17	18	100.0	600	6	CQ335104	CQ335104 Sequence
18	18	100.0	636	6	BD097037	BD097037 A BH4 fus
19	18	100.0	702	4	AY005131	AY005131 Oryctolag

c 20	18	100.0	702	6	BD084108	BD084108 Method of
c 21	18	100.0	702	6	BD102202	BD102202 Method fo
c 22	18	100.0	702	9	BT007208	BT007208 Homo sapi
c 23	18	100.0	702	12	BT008248	BT008248 Synthetic
c 24	18	100.0	723	9	HSU72398	U72398 Human Bcl-x
c 25	18	100.0	737	6	AR054022	AR054022 Sequence
c 26	18	100.0	737	6	AR172595	AR172595 Sequence
c 27	18	100.0	737	6	IS2012	IS2012 Sequence 7
c 28	18	100.0	737	6	AR371662	AR371662 Sequence
c 29	18	100.0	737	6	AR380913	AR380913 Sequence
c 30	18	100.0	737	9	HSBCLXS	Z23116 H sapiens b
c 31	18	100.0	747	6	AX127722	AX127722 Sequence
c 32	18	100.0	926	6	AR054021	AR054021 Sequence
c 33	18	100.0	926	6	AR118504	AR118504 Sequence
c 34	18	100.0	926	6	AR124952	AR124952 Sequence
c 35	18	100.0	926	6	AR144311	AR144311 Sequence
c 36	18	100.0	926	6	AR172594	AR172594 Sequence
c 37	18	100.0	926	6	BD243042	BD243042 Antisense
c 38	18	100.0	926	6	CQ765842	CQ765842 Sequence
c 39	18	100.0	926	6	E58777	E58777 Screening m
c 40	18	100.0	926	6	IS2011	IS2011 Sequence 5
c 41	18	100.0	926	6	AR371661	AR371661 Sequence
c 42	18	100.0	926	6	AR380885	AR380885 Sequence
c 43	18	100.0	926	6	AX839772	AX839772 Sequence
c 44	18	100.0	926	6	AX925686	AX925686 Sequence
c 45	18	100.0	926	9	HSBCLXL	Z23115 H sapiens b

ALIGNMENTS

RESULT 1  
BD235153  
LOCUS BD235153 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235153  
VERSION BD235153.1 GI:33044923  
KEYWORDS JP 2002519048-A/5.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 5 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/5  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGTCCTGTTCTCTTCCAC 18  
|||||

```

Db      1 AGTCCTGTTCTCTCCAC 18

RESULT 2
LOCUS      BD235168                18 bp    DNA          linear    PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235168
VERSION     BD235168.1 GI:33044938
KEYWORDS   JP 2002519048-A/20.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 20 02-JUL-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/20
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125,PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
FT Key Location/Qualifiers
FT misc binding (1)..(6)
FT misc binding (8)..(9)
FT misc binding (10)..(12)
FT misc binding (13)..(18).
FEATURES
source
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTCCAC 18
Db      1 AGTCCTGTTCTCTCCAC 18

RESULT 3
LOCUS      CQ727769/c              512 bp    DNA          linear    PAT 03-FEB-2004
DEFINITION Sequence 13703 from Patent WO02068579.
ACCESSION  CQ727769
VERSION     CQ727769.1 GI:42294740
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL    Patent: WO 02068579-A 13703 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES
source
Location/Qualifiers

Db      1 AGTCCTGTTCTCTCCAC 18

RESULT 4
LOCUS      CQ113695                555 bp    DNA          linear    PAT 21-JAN-2004
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION  CQ113695
VERSION     CQ113695.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
JOURNAL    Patent: WO 0157272-A 22554 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTCCAC 18
Db      460 AGTCCTGTTCTCTCCAC 477

RESULT 5
LOCUS      CQ152574                555 bp    DNA          linear    PAT 21-JAN-2004
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION  CQ152574
VERSION     CQ152574.1 GI:41159924
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL    Patent: WO 0157276-A 22596 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"

```

/db xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL  
= 4.7-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN  
HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION  
0.00e+00"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18

Db 460 AGTCCTGTTCTCTCCAC 477

## RESULT 6

LOCUS CQ185831 555 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 17227 from Patent WO0157274.

ACCESSION CQ185831

VERSION CQ185831.1 GI:41180846

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nuclear acid probes useful for  
analysis of gene expression in human heart

Patent: WO 0157274-A 17227 09-AUG-2001;

Neomica, Inc. (US)

FEATURES

## source

Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =

1.4-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN HIT:

BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18

Db 460 AGTCCTGTTCTCTCCAC 477

## RESULT 7

LOCUS CQ235904 555 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 22743 from Patent WO0157273.

ACCESSION CQ235904

VERSION CQ235904.1 GI:41219182

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO

3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US

60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03

August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000

(03.10.00)<150> US 60/236,359<151> 27 September 2000

(27.09.00)<150> US 60/234,687<151> 21 September 2000

(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
Patent: WO 0157273-A 22743 09-AUG-2001;  
Neomica, Inc. (US)

## JOURNAL

Neomica, Inc. (US)

## FEATURES

Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL

= 1.7-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18

Db 460 AGTCCTGTTCTCTCCAC 477

## RESULT 8

LOCUS CQ273477 555 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 21738 from Patent WO0157277.

ACCESSION CQ273477

VERSION CQ273477.1 GI:41246081

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nuclear acid probes useful for

analysis of gene expression in human fetal liver

Patent: WO 0157277-A 21738 09-AUG-2001;

Neomica, Inc. (US)

FEATURES

## source

Location/Qualifiers

1..555

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL

= 3.5-SWISSPROT HIT: Q07817, EVALUATION 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUATION 0.00e+00-NT HIT: U72398.1, EVALUATION

0.00e+00"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18

Db 460 AGTCCTGTTCTCTCCAC 477

## RESULT 9

LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 21963 from Patent WO0186003.

ACCESSION CQ310858

VERSION CQ310858.1 GI:41271435

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1

**REFERENCE**  
**AUTHORS** Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung  
**JOURNAL** Patent: WO 0186003-A 21963 15-NOV-2001;  
**FEATURES** Location/Qualifiers  
**source** 1..555  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"  
**ORIGIN**  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCCTGTTCTCTCCAC 18  
|||||  
Db 460 AGTCCTGTTCTCTCCAC 477  
  
**RESULT 10**  
**LOCUS** CQ347773 555 bp DNA linear PAT 23-JAN-2004  
**DEFINITION** Sequence 21867 from Patent WO0157275.  
**ACCESSION** CQ347773  
**VERSION** CQ347773.1 GI:41296844  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
**AUTHORS** Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain  
**JOURNAL** Patent: WO 0157275-A 21867 09-AUG-2001;  
**FEATURES** Location/Qualifiers  
**source** 1..555  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL = 1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"  
**ORIGIN**  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCCTGTTCTCTCCAC 18  
|||||  
Db 460 AGTCCTGTTCTCTCCAC 477  
  
**RESULT 11**  
**LOCUS** CQ100639 600 bp DNA linear PAT 21-JAN-2004  
**DEFINITION** Sequence 9498 from Patent WO0157272.  
**ACCESSION** CQ100639  
**VERSION** CQ100639.1 GI:41069665  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
**AUTHORS** Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta  
**JOURNAL** Patent: WO 0157272-A 9498 09-AUG-2001;  
**FEATURES** Location/Qualifiers  
**source** 1..600  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99"  
**ORIGIN**  
Query Match 100.0%; Score 18; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCCTGTTCTCTCCAC 18  
|||||  
Db 479 AGTCCTGTTCTCTCCAC 496  
  
**RESULT 12**  
**LOCUS** CQ139631 600 bp DNA linear PAT 21-JAN-2004  
**DEFINITION** Sequence 9653 from Patent WO0157276.  
**ACCESSION** CQ139631  
**VERSION** CQ139631.1 GI:41097003  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
**AUTHORS** Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow  
**JOURNAL** Patent: WO 0157276-A 9653 09-AUG-2001;  
**FEATURES** Location/Qualifiers  
**source** 1..600  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 4.7"  
**ORIGIN**  
Query Match 100.0%; Score 18; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCCTGTTCTCTCCAC 18  
|||||  
Db 479 AGTCCTGTTCTCTCCAC 496  
  
**RESULT 13**  
**LOCUS** CQ175964 600 bp DNA linear PAT 21-JAN-2004  
**DEFINITION** Sequence 7360 from Patent WO0157274.  
**ACCESSION** CQ175964  
**VERSION** CQ175964.1 GI:41170703  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
**AUTHORS** Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for

analysis of gene expression in human heart  
Patent: WO 0157274-A 7360 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source  
1. .600  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP to AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"  
ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCCTGTTCTCTCCAC 18  
|||||  
Db 479 AGTCCTGTTCTCTCCAC 496  
RESULT 14  
CQ222999  
LOCUS  
DEFINITION  
Sequence 9838 from Patent WO0157273.  
CQ222999  
ACCESSION  
VERSION  
CQ222999.1 GI:41205280  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Penn.S.G., Hanzel,D.K., Chen,W. and Rank, D.R.  
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
3<150> US 60/180.312<151> 04 February 2000 (04.02.00)<150> US  
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
(03.10.00)<150> US 60/236,359<151> 27 September 2000  
(27.09.00)<150> US 60/234,687<151> 21 September 2000  
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
Patent: WO 015723-A 9838 09-AUG-2001;  
Aeomeica, Inc. (US)  
Location/Qualifiers  
1. .600  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9~EXPRESSED IN ADULT LIVER, SIGNAL  
= 1.7"

Query Match	100.0%;	Score 18;	DB 6;	Length 600;
Best Local Similarity	100.0%;	Pred. NO. 2e+02;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 AGTCCTGTTCTCTCCAC 18 			
Dd	479 AGTCCTGTTCTCTCCAC 496 			
RESULT 15				
CQ260961				
LOCUS	CQ260961	600 bp	DNA	linear
DEFINITION	Sequence 9222 from Patent WO0157277.			
ACCESSION	CQ260961			
VERSION	CQ260961.1	GI:41233441		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169a-5  
Perfect score: 18  
Sequence: 1 agtcctgtctcttcac 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	AAZ46975 Bcl-Xl mr
2	18	100.0	555	4	ABA73433 Human foe
3	18	100.0	555	4	AAI53868 Probe #22
4	18	100.0	555	4	ABA38761 Probe #17
5	18	100.0	555	4	AAK48039 Human bon
6	18	100.0	555	4	AAK21876 Human bra
7	18	100.0	555	4	ABS47753 Human liv
8	18	100.0	555	6	ABS21972 Human gen
9	18	100.0	559	12	ACH73889 Human gen
10	18	100.0	564	12	ACH87595 Human gen
11	18	100.0	600	4	ABA60917 Human foe
12	18	100.0	600	4	AAI40812 Probe #94
13	18	100.0	600	4	ABA28894 Probe #73
14	18	100.0	600	4	AAK35096 Human bon
15	18	100.0	600	4	AAK09207 Human bra
16	18	100.0	600	4	ABS34848 Human liv
17	18	100.0	600	6	ABS09558 Human gen
c 18	18	100.0	636	4	AAH48169 Mutant bc
c 19	18	100.0	702	5	AAH43464 cDNA clon
c 20	18	100.0	702	12	ADM45994 Human apo
c 21	18	100.0	737	2	AAQ81699 Human thy

c 22	18	100.0	737	10	ABZ83507 Toxicolog
c 23	18	100.0	737	11	ADI32132 Human cDN
c 24	18	100.0	739	12	ADG65218 Human Bcl
c 25	18	100.0	747	4	AAF30926 Human Bcl
c 26	18	100.0	747	12	ADG65209 Human Bcl
c 27	18	100.0	926	2	AAQ81698 Human thy
c 28	18	100.0	926	2	AAQ40079 Bcl-XL ge
c 29	18	100.0	926	3	AAZ93614 Bcl-x gen
c 30	18	100.0	926	4	AAI515189 Human Bcl
c 31	18	100.0	926	4	AAC90810 Human Bcl
c 32	18	100.0	926	6	ABK84766 Human cDN
c 33	18	100.0	926	8	ABT16641 Human bcl
c 34	18	100.0	926	10	ADBS6779 Human bcl
c 35	18	100.0	926	10	AAD64187 Human bcl
c 36	18	100.0	926	11	ADI32104 Human cDN
c 37	18	100.0	926	12	ADH52630 Human ant
c 38	18	100.0	926	12	ADO19990 Human PRO
c 39	18	100.0	926	12	ADP13351 Renal cel
c 40	18	100.0	1236	5	AAS00247 Bcl-Xl-DT
c 41	18	100.0	1455	5	AAS00250 LFN-Bcl-X
c 42	18	100.0	2386	10	ADG89403 Cancer de
c 43	18	100.0	2386	12	ADN04260 Antipsori
c 44	18	100.0	2575	12	ADO19866 Human PRO
c 45	18	100.0	7372	2	AAZ33182 Base Sequ

ALIGNMENTS

RESULT 1  
AAZ46975

ID AAZ46975 standard; DNA; 18 BP.

XX AAZ46975;

DT 14-APR-2000 (first entry)

XX Bcl-Xl mRNA specific antisense oligo E.

XX Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
XX lung; bladder; bcl-2; vascular lesion; antisense; ss.

XX Homo sapiens.

XX WC200001393-A2.

PD 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

XX New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX Claim 1; Fig 1; 69pp; English.

XX The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
 |||||  
 Db 1 AGTCCTGTTCTCTTCCAC 18

## RESULT 2

ABA73433  
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;

XX DT 01-FEB-2002 (first entry)

XX DE Human foetal liver single exon nucleic acid probe #21738.

XX KW Human, foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human fetal liver.

XX PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring

XX CC human gene expression in a sample derived from human foetal liver. The

XX CC single exon nucleic acid probes may be used for predicting, measuring and

XX CC displaying gene expression in samples derived from human fetal liver. The

XX CC present sequence is a single exon nucleic acid probe of the invention.

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
 |||||  
 Db 460 AGTCCTGTTCTCTTCCAC 477

## RESULT 3

AAI53868  
 ID AAI53868 standard; DNA; 555 BP.

XX AC AAI53868;

XX DT 17-OCT-2001 (first entry)

XX DE Probe #22554 used to measure gene expression in human placenta sample.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;

XX KW genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human placenta.

XX PS Claim 25; SEQ ID NO 22554; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP).

XX CC The present sequence is one such probe. The probes are useful for

XX CC producing a microarray for predicting, measuring and displaying gene

XX CC expression in samples derived from human placenta. The probes are useful

XX CC for antenatal diagnosis of human genetic disorders

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
 |||||  
 Db 460 AGTCCTGTTCTCTTCCAC 477

## RESULT 4

ABA38761  
 ID ABA38761 standard; DNA; 555 BP.

XX AC ABA38761;

XX DT 23-JAN-2002 (first entry)

XX DE Probe #17227 for gene expression analysis in human heart cell sample.

XX KW Human; gene expression; heart; microarray; vascular system; probe;

XX KW cardiovascular disease; hypertension; cardiac arrhythmia;

XX KW congenital heart disease; ss.



```
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-488899/53.
XX
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
XX
PS Claim 4; SEQ ID NO 17227; 530pp; English.
XX
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
Db |||||
460 AGTCCTGTTCTCTCCAC 477

RESULT 5
AAK48039
ID AAK48039 standard; DNA; 555 BP.
XX
XX
AC AAK48039;
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157276-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-483446/52.
XX
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTCCAC 18
Db |||||
460 AGTCCTGTTCTCTCCAC 477

RESULT 6
AAK21876
ID AAK21876 standard; DNA; 555 BP.
XX
XX
AC AAK21876;
XX
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 21867.
XX
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157275-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-483446/52.
XX
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
```

XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention

XX

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 AGTCCTGTTCTCTTCCAC 18

DB 460 AGTCCTGTTCTCTTCCAC 477

RESULT 7

ABS47753

ID ABS47753 standard; DNA; 555 BP.

XX

AC ABS47753;

XX

XX 25-FEB-2003 (first entry)

XX

DE Human liver single exon probe, SEQ ID No 22743.

XX

XX Human; single exon nucleic acid probe; liver; cirrhosis;

KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;

KW coronary heart disease; ss.

XX

OS Homo sapiens.

XX

XX WO200157273-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000664.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-00608408.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-0234687P.

PR

XX 27-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI

XX WPI; 2001-488998/53.

DR

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human adult liver.

XX

XX Claim 4; SEQ ID NO 22743; 658pp; English.

PS

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

CC measuring human gene expression in a sample derived from human adult

CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridises at high

CC stringency to a nucleic acid molecule expressed in the human adult liver.

CC (i) may be used for predicting, measuring and displaying gene expression

CC in samples derived from human adult liver. The genes identified may be

CC involved in genetic liver diseases such as cirrhosis,

CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

CC associated with coronary heart disease. ABS25011-ABS51005 represent human

CC

CC liver single exon nucleic acid probes of the invention. Note: The

CC sequence information for this patent does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 AGTCCTGTTCTCTTCCAC 18

DB 460 AGTCCTGTTCTCTTCCAC 477

RESULT 8

ABS21972

ID ABS21972 standard; DNA; 555 BP.

XX

AC ABS21972;

XX

XX 19-AUG-2002 (first entry)

XX

DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.

XX

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioliomyomatosis; Karagener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease; open reading frame; ORF.

XX

OS Homo sapiens.

XX

XX WO200186003-A2.

PN

XX 15-NOV-2001.

PD

XX 30-JAN-2001; 2001WO-US000665.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-00608408.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-0234687P.

PR

XX 27-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI

XX WPI; 2002-114183/15.

DR

XX

PT Spatially-addressable set of single exon nucleic acid probes, used to

XX measure gene expression in human lung samples.

XX

XX Claim 4; SEQ ID NO 21963; 634pp; English.

PS

XX The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC

CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
 |||||  
 Db 460 AGTCCTGTTCTCTTCCAC 477

## RESULT 9

ACH73889  
 ID ACH73889 standard; DNA; 559 BP.

XX AC ACH73889;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #7084.

XX KW Human; probe; ss; gene expression; single exon probe; microarray;  
 XX KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX PA (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX PI Penn SG, Rank DR, Hanzel DK;

XX DR WPI; 2004-119264/12.

XX PT New human genome-derived single exon nucleic acid probes useful for human

XX gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for  
 XX surveying tissues.

XX PS Claim 15; SEQ ID NO 7084; 80pp; English.

XX CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expressions, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC a method of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above). The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The present sequence is a human  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX SQ Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 559;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
 |||||  
 Db 55 AGTCCTGTTCTCTTCCAC 72

## RESULT 10

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX AC ACH87595;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #20790.

XX KW Human; probe; ss; gene expression; single exon probe; microarray;  
 XX KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX

```
PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTCCTGTTCTCTTCCAC 18
Db 460 AGTCCTGTTCTCTTCCAC 477
RESULT 11
ABA60917
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #9222.
DE
```

---

```
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW Homo sapiens.
OS
XX WO200157277-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX
XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTCCTGTTCTCTTCCAC 18
Db 479 AGTCCTGTTCTCTTCCAC 496
RESULT 12
AAI40812
ID AAI40812 standard; DNA; 600 BP.
XX
XX AAI40812;
XX
XX 17-OCT-2001 (first entry)
DT
XX
XX Probe #9498 used to measure gene expression in human placenta sample.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200157272-A2.
PN
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
```

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488897/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
PT
XX Claim 25; SEQ ID NO 9498; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
CC
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGTCCTGTTCTCTTCCAC 18
Db |||||||||||||||
479 AGTCCTGTTCTCTTCCAC 496

RESULT 13
ABA28894
ID ABA28894 standard; DNA; 600 BP.
XX
AC ABA28894;
XX
XX 23-JAN-2002 (first entry)
XX
DE Probe #7360 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PP 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488899/53.
DR
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX

```

---

```

PS Claim 1; SEQ ID NO 7360; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGTCCTGTTCTCTTCCAC 18
Db |||||||||||||||
479 AGTCCTGTTCTCTTCCAC 496

RESULT 14
AAK35096
ID AAK35096 standard; DNA; 600 BP.
XX
AC AAK35096;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PP 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488900/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
PT
XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
SQ

```

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 1 AGTCCTGTTCTCTCCAC 18  
| | | | | | | | | | | | | | | | | |  
Db 479 AGTCCTGTTCTCTCCAC 496

## RESULT 15

AAK09207  
ID AAK09207 standard; DNA; 600 BP.

XX AC AAK09207;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe SEQ ID NO: 9198.

XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KW ss.

XX OS Homo sapiens.

XX PN WO200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000667.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human  
XX brains.

XX PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid  
XX probes which are derived from genomic sequences expressed in the human  
XX brain. They can be used to measure gene expression in brain cell samples,  
XX which may enable the diagnosis and improved treatment of nervous system  
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
XX epilepsy and cancers. The present sequence is one of the probes of the  
XX invention

XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 1 AGTCCTGTTCTCTCCAC 18  
| | | | | | | | | | | | | | | | | |  
Db 479 AGTCCTGTTCTCTCCAC 496

Search completed: February 4, 2005, 21:52:42  
Job time : 233.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-5  
Perfect score: 18  
Sequence: 1 agtcctgtcttctccac 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gsl1.\*  
9: gb\_gsl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	279	2	AW247015
C 2	18	100.0	382	4	BM855440
C 3	18	100.0	395	4	BT030877
C 4	18	100.0	421	4	BM844286
C 5	18	100.0	421	6	CF145335
C 6	18	100.0	433	4	BT022254
C 7	18	100.0	474	7	CN422261
C 8	18	100.0	490	4	BG746308
C 9	18	100.0	503	1	AT283063
C 10	18	100.0	503	4	BM857244
C 11	18	100.0	542	7	CN422262
C 12	18	100.0	543	5	BX487587
C 13	18	100.0	560	6	CD675630
C 14	18	100.0	577	6	CF131978
C 15	18	100.0	584	1	AL134785
C 16	18	100.0	587	2	BE871836
C 17	18	100.0	596	2	AW732926
C 18	18	100.0	602	7	CN422268
C 19	18	100.0	616	2	BE783664
C 20	18	100.0	616	6	CF132307
C 21	18	100.0	619	2	BF038769
C 22	18	100.0	624	6	CF131456
C 23	18	100.0	632	7	CN422264
C 24	18	100.0	635	4	BI489889

C 25	18	100.0	657	2	BE207063
C 26	18	100.0	671	2	AW814739
C 27	18	100.0	688	4	BG708652
C 28	18	100.0	702	6	CF125275
C 29	18	100.0	704	4	BI561500
C 30	18	100.0	707	6	CD636467
C 31	18	100.0	711	2	BE535474
C 32	18	100.0	720	6	CD636470
C 33	18	100.0	726	2	BF116000
C 34	18	100.0	727	2	BE782921
C 35	18	100.0	731	4	BI766475
C 36	18	100.0	735	4	BI522819
C 37	18	100.0	735	6	CD641746
C 38	18	100.0	751	2	BE734566
C 39	18	100.0	776	2	BF529410
C 40	18	100.0	798	7	CK000319
C 41	18	100.0	821	5	BQ932013
C 42	18	100.0	830	7	CF619432
C 43	18	100.0	831	7	CO247250
C 44	18	100.0	834	4	BI550492
C 45	18	100.0	836	4	BM018295

ALIGNMENTS

RESULT 1  
AW247015/c  
LOCUS 2822471.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:282471 5',  
DEFINITION mRNA sequence.  
ACCESSION AW247015  
VERSION AW247015.1 GI:6590008  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 279)  
NIT-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Other ESTs: 2822471.3prime  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rc@mail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu  
Plate: LHCW9 row: H column: 24  
High quality sequence stop: 199.  
Location/Qualifiers  
1. .279  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:282471"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
|||||  
Db 161 AGTCCTGTTCTCTTCCAC 144

## RESULT 2

BM855440/c  
LOCUS K-EST0138319 S21SNU520 Homo sapiens cDNA clone S21SNU520-67-G02 5',  
DEFINITION mRNA sequence.

ACCESSION BM855440  
VERSION BM855440.1 GI:19211825  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 382)

## REFERENCE

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.

## TITLE

21C Frontier Korean EST Project 2001

## JOURNAL

Unpublished (2002)

## COMMENT

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 67 row: G column: 02  
High quality sequence stop: 382.

## FEATURES

source

1..382

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S21SNU520-67-G02"  
/sex="P"

/tissue\_type="Stomach"  
/cell\_type="Floating aggregates"  
/lab\_host="Top10F"

/lab\_line="SNU-520"

/notes="Organ: Stomach; Vector: pTZ19RPL; Site 1: EcoRI;  
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transposition of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
|||||  
Db 341 AGTCCTGTTCTCTTCCAC 324

## RESULT 3

BI030877/c

LOCUS IL5-MT0262-290301-406-g10 MT0262 Homo sapiens linear EST 14-JUN-2001

DEFINITION BI030877

ACCESSION BI030877.1 GI:14437507

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 395)

REFERENCE Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

AUTHORS Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?c1=IL5&t2=IL5-MT0262-  
290301-406-g10&t3=2001-03-29&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 346.  
Location/Qualifiers  
1..395  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="MT0262"  
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 395;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCCTGTTCTCTTCCAC 18  
|||||  
Db 369 AGTCCTGTTCTCTTCCAC 352

## RESULT 4

BM844286/c

LOCUS K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',  
DEFINITION

Query Match 100.0%; Score 18; DB 4; Length 395;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

mRNA sequence.
ACCESSION   BM844286
VERSION     BM844286.1  GI:19200695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 421)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 63 row: B column: 03
            High quality sequence stop: 421.
FEATURES   Location/Qualifiers
            1..421
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="S12SNU216-63-B03"
                /sex="F"
                /tissue_type="Lymph node"
                /cell_type="Epithelial"
                /lab_host="SNU-216"
                /clone_lib="S12SNU216"
                /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10+ by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCTGTTCTCTTCCAC 18
    |||||
Db 108 AGTCTGTTCTCTTCCAC 91

RESULT 5
CF145335/C
LOCUS       CF145335
DEFINITION UI-HF-CBO-asn-f-06-0-UI.r1 NIH MGC_210 Homo sapiens cDNA clone
IMAGE:30569057 5', mRNA sequence.
ACCESSION   CF145335
VERSION     CF145335.1  GI:33260779
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 421)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 63 row: B column: 03
            High quality sequence stop: 421.
FEATURES   Location/Qualifiers
            1..421
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="S12SNU216-63-B03"
                /sex="F"
                /tissue_type="Lymph node"
                /cell_type="Epithelial"
                /lab_host="SNU-216"
                /clone_lib="S12SNU216"
                /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10+ by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCTGTTCTCTTCCAC 18
    |||||
Db 108 AGTCTGTTCTCTTCCAC 91

RESULT 6
BI022254
LOCUS       BI022254
DEFINITION CM3-MT0294-170101-631-c01 MT0294 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI022254
VERSION     BI022254.1  GI:14428884
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
AUTHORS    Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Tim Ratliff
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/humanfl.html
            Seq primer: pYX-5.
FEATURES   Location/Qualifiers
            1..421
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:30569057"
                /tissue_type="CNCAP(3)T-225 cell line"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH_MGC_210"
                /note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: EcoR I;
                Site_2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated
                with EcoR I adaptor, digested with Not I and then cloned
                directionally into pT7T3 Pac vector. The library tag
                sequence located between the Not I site and the polyA tail
                is CCCAC. Tissue was provided by Tim Ratliff."
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCTGTTCTCTTCCAC 18
    |||||
Db 102 AGTCTGTTCTCTTCCAC 85

RESULT 6
BI022254
LOCUS       BI022254
DEFINITION CM3-MT0294-170101-631-c01 MT0294 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI022254
VERSION     BI022254.1  GI:14428884
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags

```

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICK Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-WT0294-  
170101-631-c01&t3=2001-01-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 433.

FEATURES  
source  
1..433  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="WT0294"  
/note="Organ: marrow; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

ORIGIN  
Query Match 100.0%; Score 18; DB 4; Length 433;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCAC 18  
Db 42 AGTCCTGTTCTCTTCAC 59

RESULT 7  
CN422261/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

17000424524125 GRN EB Homo sapiens CDNA 5', mRNA sequence.  
CN422261  
CN422261.1 GI:47409855  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Mursage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert length: 474 Std Error: 0.00.

FEATURES  
source  
1..474  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_lib="GRN EB"  
/note="oligo dt primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from h9 cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN  
Query Match 100.0%; Score 18; DB 7; Length 474;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCAC 18  
Db 163 AGTCCTGTTCTCTTCAC 146

RESULT 8  
BG746308/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

602703549F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4856725 5',  
mRNA sequence.  
BG746308  
BG746308.1 GI:14056961  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgc.mci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCMI708 row: a column: 14  
High quality sequence stop: 464.

FEATURES  
source  
1..490  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4856725"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 15"  
/note="Organ: colon; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN  
Query Match 100.0%; Score 18; DB 4; Length 490;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCAC 18  
Db 242 AGTCCTGTTCTCTTCAC 225

RESULT 9  
 A1283063 503 bp mRNA linear EST 29-JAN-1999  
 LOCUS qm2c06.x1 Soares placenta 8to9weeks 2NBHP8to9w Homo sapiens CDNA  
 DEFINITION clone IMAGE:1893322 3', similar to SW:BCIX\_HUMAN Q07817 APOPTOSIS  
 REGULATOR BCL-X., mRNA sequence.

ACCESSION A1283063  
 VERSION A1283063.1 GI:3921296  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 503)  
 REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](mailto:infoimage.llnl.gov)) for further information.  
 Insert Length: 1323 Std Error: 0.00  
 Seq Primer: -40UP from Gibco  
 High quality sequence stop: 440.

FEATURES  
 source  
 1..503  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1893322"  
 /dev\_stages="two placentae: one from 8 weeks and another  
 from 9 weeks post conception"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares placenta 8to9weeks 2NBHP8to9w"  
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a  
 modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTGAAGTGGAGCGCCGCGATTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified p773 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M.Fatima Bonaldo."

ORIGIN  
 Query Match 100.0%; Score 18; DB 1; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCCAC 18  
 |||  
 Db 458 AGTCCTGTTCTCTTCCAC 441

RESULT 10  
 BM857244/c  
 LOCUS K-EST0141477 S21SNUS20 Homo sapiens CDNA clone S21SNUS20-78-F09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BM857244  
 VERSION BM857244.1 GI:19213643  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 503)  
 REFERENCE Oh,K.J., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)

COMMENT  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: [yongsung@mail.kribb.re.kr](mailto:yongsung@mail.kribb.re.kr)  
 Plate: 78 row: F column: 09  
 High quality sequence stop: 503.  
 Location/Qualifiers  
 1..503  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S21SNUS20-78-F09"  
 /sex="F"  
 /tissue\_type="Stomach"  
 /cell\_type="floating aggregates"  
 /cell\_line="SNU-520"  
 /lab\_host="Top10F"  
 /clone\_lib="S21SNUS20"  
 /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tabacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTCCTGTTCTCTTCCAC 18  
 |||  
 Db 109 AGTCCTGTTCTCTTCCAC 92

RESULT 11  
 CN422262/c  
 LOCUS CN422262  
 DEFINITION 17000424524143 GRN\_EB Homo sapiens CDNA 5', mRNA sequence.  
 ACCESSION CN422262  
 VERSION CN422262.1 GI:47409856  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 542)  
 REFERENCE Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,  
 AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,  
 Lebkowski,J and Stanton,L.W.  
 TITLE Transcriptome characterization elucidates signaling networks that  
 control human ES cell growth and differentiation  
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
 COMMENT Contact: Brandenberger R  
 Regenerative Medicine  
 Geron Corporation  
 230 Constitution Drive, Menlo Park, CA 94025, USA  
 Tel: 650 473 8658  
 Fax: 650 473 7760  
 Email: [rbrandenberger@geron.com](mailto:rbrandenberger@geron.com)



```

VERSION      CF131978.1  GI:33214777
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      1 (bases 1 to 577)
              Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE        Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL      Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477
PUBMED       889548
COMMENT      Contact: Soares, MB
              Coordinated Laboratory for Computational Genomics
              University of Iowa
              375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: bento-soares@uiowa.edu
              Tissue Procurement: Mary Hendrix
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Distribution information can be found at
              http://genome.uiowa.edu/distribution/humanfl.html
              Seq primer: pYX-5.

FEATURES     source
              Location/Qualifiers
                1..577
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3053743"
                /tissue_type="Chondrosarcoma Lung Metastasis cell lines"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH_MGC_215"
                /note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
                Site 2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated
                with EcoR I adaptor, digested with Not I and then cloned
                directionally into pYX-Asc vector. The library tag
                sequence located between the Not I site and the polyA tail
                is GATAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 577;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTTCCAC 18
        |||||
Db      248 AGTCCTGTTCTCTTCCAC 231

RESULT 15
AL134785/c
LOCUS       AL134785
DEFINITION DKFP547K2090 r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
ACCESSION  AL134785
VERSION     AL134785.1  GI:8602972
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and

JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
              This is the 5' sequence of the clone insert
              Clone from S. Wiemann. Molecular Genome Analysis, German Cancer
              Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
              Heidelberg/Germany) within the cDNA sequencing consortium of the
              German Genome Project.
              No sl sequence available.
              This clone (DKFZp547K2090) is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES     source
              Location/Qualifiers
                1..584
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFZp547K2090"
                /tissue_type="brain"
                /dev_stage="fetal"
                /lab_host="Xi-2blue"
                /clone_lib="347 (synonym: hfbr1)"
                /note="vector: pAMPI; Site 1: NotI; Site 2: SalI"

ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGTCCTGTTCTCTTCCAC 18
        |||||
Db      138 AGTCCTGTTCTCTTCCAC 121

Search completed: February 5, 2005, 08:11:42
Job time : 2151.2 secs

```

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 , Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-6  
Perfect score: 18  
Sequence: 1 ctttactgtgcatggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644845745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hug.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pi.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235154
2	18	100.0	18	6	BD235170
3	18	100.0	512	6	C0727769
4	18	100.0	555	6	C0113695
5	18	100.0	555	6	C0152574
6	18	100.0	555	6	C0185831
7	18	100.0	555	6	C0235904
8	18	100.0	555	6	C0273477
9	18	100.0	555	6	C0310858
10	18	100.0	555	6	C0347773
11	18	100.0	600	6	C0106639
12	18	100.0	600	6	C0139631
13	18	100.0	600	6	C0175964
14	18	100.0	600	6	C0222999
15	18	100.0	600	6	C0260961
16	18	100.0	600	6	C0298444
17	18	100.0	600	6	C0335104
18	18	100.0	636	6	BD097037
19	18	100.0	702	6	BD084108

C 20	18	100.0	702	6	BD102202
C 21	18	100.0	702	9	BT007208
C 22	18	100.0	702	12	BT008248
C 23	18	100.0	723	9	HSU72398
C 24	18	100.0	737	6	AR054022
C 25	18	100.0	737	6	AR172595
C 26	18	100.0	737	6	IS2012
C 27	18	100.0	737	6	AR371662
C 28	18	100.0	737	6	AR380913
C 29	18	100.0	737	9	HSBCLXS
C 30	18	100.0	747	6	AX127722
C 31	18	100.0	926	6	AR054021
C 32	18	100.0	926	6	AR118504
C 33	18	100.0	926	6	AR124952
C 34	18	100.0	926	6	AR144311
C 35	18	100.0	926	6	AR172594
C 36	18	100.0	926	6	BD243042
C 37	18	100.0	926	6	CQ765842
C 38	18	100.0	926	6	ES8777
C 39	18	100.0	926	6	IS2011
C 40	18	100.0	926	6	AR371661
C 41	18	100.0	926	6	AR380885
C 42	18	100.0	926	6	AX839772
C 43	18	100.0	926	6	AX925686
C 44	18	100.0	926	9	HSBCLXL
C 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1  
LOCUS BD235154 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235154  
VERSION BD235154.1 GI:33044924  
KEYWORDS JP 2002519048-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein,C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 6 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/6  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTACTGTGCGCATGGG 18  
|||||||

```

Db          1 CTTTACTGCTGCCATGGG 18
RESULT 2
BD235170
LOCUS      18 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235170
VERSION     BD235170.1 GI:33044940
KEYWORDS   JP 2002519048-A/22.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stein,C.A.
TITLE     Oligonucleotide inhibitors of bcl-xL
JOURNAL   Patent: JP 2002519048-A 22 02-JUL-2002;
          THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS JP 2002519048-A/22
          PN JP 2002519048-A/22
          PD 02-JUL-2002
          PF 02-JUL-1999 JP 2000557839
          PR 02-JUL-1998 US 09/109614
          PI CY A STEIN
          PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125,PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PROPYNYL dc
CC PROPYNYL dt
CC PROPYNYL dt
CC PROPYNYL dt
CC PROPYNYL dt
CC PROPYNYL dt
CC PROPYNYL dt
CC Key
FH Location/Qualifiers
FT (1)..(4)
FT misc_binding
FT (9)..(10)
FT misc_binding
FT (12)..(13)
FT misc_binding
FT (15)..(18)
FT modified_base
FT (1)..(1)
FT modified_base
FT (2)..(4)
FT modified_base
FT (6)..(6)
FT modified_base
FT (7)..(7)
FT modified_base
FT (9)..(9)
FT modified_base
FT (10)..(10)
FT modified_base
FT (12)..(13)
FT modified_base
FT (15)..(15)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 1 CTTTACTGCTGCCATGGG 18
RESULT 3
CQ727769/c
LOCUS      512 bp DNA linear PAT 03-FEB-2004
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  CQ727769
VERSION     CQ727769.1 GI:42294740
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE     Kits, such as nucleic acid arrays, comprising a majority of
          humanexons or transcripts, for detecting expression and other uses
          thereof
JOURNAL   Patent: WO 02068579-A 13703 06-SEP-2002;
          PE Corporation (NY) (US)
FEATURES
source
1..512
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 5
CQ152574
LOCUS      555 bp DNA linear PAT 21-JAN-2004
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  CQ152574
VERSION     CQ152574.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human placenta
JOURNAL   Patent: WO 0157272-A 22554 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/Note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 5
CQ152574
LOCUS      555 bp DNA linear PAT 21-JAN-2004
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  CQ152574
VERSION     CQ152574.1 GI:41083565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human placenta
JOURNAL   Patent: WO 0157272-A 22554 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES
source
1..555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/Note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321

```



```

VERSION      CQ152574.1  GI:41159924
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 22596 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
                = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||+|||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 6
CQ185831
LOCUS       CQ185831             555 bp DNA linear PAT 21-JAN-2004
DEFINITION  Sequence 17227 from Patent WO0157274.
ACCESSION   CQ185831
VERSION     CQ185831.1  GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 17227 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
                1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN HIT:
                BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||+|||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 7
CQ235904
LOCUS       CQ235904             555 bp DNA linear PAT 21-JAN-2004
DEFINITION  Sequence 22743 from Patent WO0157273.

```

```

ACCESSION    CQ235904
VERSION      CQ235904.1  GI:41219182
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 22743 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
                = 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
    |||||+|||||
Db 304 CTTTACTGCTGCCATGGG 321

RESULT 8
CQ273477
LOCUS       CQ273477             555 bp DNA linear PAT 23-JAN-2004
DEFINITION  Sequence 21738 from Patent WO0157277.
ACCESSION   CQ273477
VERSION     CQ273477.1  GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     source
              1..555
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
                = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST_HUMAN
                HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

```

```

Db      304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 9
LOCUS      CQ310858                      555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION     CQ310858.1 GI:41271435
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 21963 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
            BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db      304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 10
LOCUS      CQ347773                      555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION  CQ347773
VERSION     CQ347773.1 GI:41296844
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 21867 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
            1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
            BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
            0.00e+00"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db      304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 11
LOCUS      CQ100639                      600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION  CQ100639
VERSION     CQ100639.1 GI:41069665
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
JOURNAL     Patent: WO 0157272-A 9498 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
            0.99"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db      304 CTTTACTGCTGCCATGGG 321
|||||
|||||

RESULT 12
LOCUS      CQ139631                      600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION  CQ139631
VERSION     CQ139631.1 GI:41097003
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL     Patent: WO 0157276-A 9653 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /notes="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
            = 4.7"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTACTGCTGCCATGGG 18
|||||
|||||

Db      323 CTTTACTGCTGCCATGGG 340
|||||
|||||

```

RESULT 13  
 LOCUS CQ175964  
 DEFINITION Sequence 7360 from Patent WO0157274.  
 ACCESSION CQ175964  
 VERSION CQ175964.1 GI:41170703  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human heart  
 JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN  
 Query Match 100.0%; Score 18; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 Db 323 CTTTACTGCTGCCATGGG 340

RESULT 14  
 LOCUS CQ222999  
 DEFINITION Sequence 9838 from Patent WO0157273.  
 ACCESSION CQ222999  
 VERSION CQ222999.1 GI:41205280  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
 (03.10.00)<150> US 60/236,359<151> 27 September 2000  
 (27.09.00)<150> US 60/234,687<151> 21 September 2000  
 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
 Molecular Dynamics Sequence Listing Engine  
 JOURNAL Patent: WO 0157273-A 9838 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL  
 = 1.7"

ORIGIN  
 Query Match 100.0%; Score 18; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 Db 323 CTTTACTGCTGCCATGGG 340

Qy 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 Db 323 CTTTACTGCTGCCATGGG 340

RESULT 15  
 LOCUS CQ260961  
 DEFINITION Sequence 9222 from Patent WO0157277.  
 ACCESSION CQ260961  
 VERSION CQ260961.1 GI:41233441  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 analysis of gene expression in human fetal liver  
 JOURNAL Patent: WO 0157277-A 9222 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL  
 = 3.5"

ORIGIN  
 Query Match 100.0%; Score 18; DB 6; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 Db 323 CTTTACTGCTGCCATGGG 340

Search completed: February 4, 2005, 23:30:40  
 Job time : 432.664 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-6  
Perfect score: 18  
Sequence: 1 cttactgctgcatggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46976 Bcl-XL MR
2	18	100.0	555	4	ABA73433 Human foe
3	18	100.0	555	4	Aa153868 Probe #22
4	18	100.0	555	4	Aba38761 Probe #17
5	18	100.0	555	4	Aak48039 Human bon
6	18	100.0	555	4	Aak21876 Human bra
7	18	100.0	555	4	ABs47753 Human liv
8	18	100.0	555	6	ABs21972 Human gen
9	18	100.0	564	12	ACH87595 Human gen
10	18	100.0	600	4	ABA60917 Human foe
11	18	100.0	600	4	Aa140812 Probe #94
12	18	100.0	600	4	ABA28894 Probe #73
13	18	100.0	600	4	Aak35096 Human bon
14	18	100.0	600	4	Aak09207 Human bra
15	18	100.0	600	4	ABs34848 Human liv
16	18	100.0	600	6	ABs09558 Human gen
17	18	100.0	636	4	AaH48169 Mutant bc
18	18	100.0	702	5	AaH43464 cDNA clon
19	18	100.0	702	12	Adm45994 Human apo
20	18	100.0	737	2	AaQ1699 Human thy
21	18	100.0	737	10	ABz83507 Toxicolog

## ALIGNMENTS

## RESULT 1

Az46976  
ID Az46976 standard; DNA; 18 BP.  
XX AC Az46976;  
XX AC  
DT 14-APR-2000 (first entry)  
XX DE Bcl-XL mRNA specific antisense oligo F.  
XX DE  
XX DE Anti-apoptotic protein; bcl-XL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX OS Homo sapiens.  
XX OS  
XX PN WO200001393-A2.  
XX PN  
PD 13-JAN-2000.  
XX PF  
PF 02-JUL-1999; 99WO-US015250.  
XX PR  
PR 02-JUL-1998; 98US-00109614.  
XX PS  
PS (UYCO ) UNIV COLUMBIA NEW YORK.  
XX PI Stein CA;  
XX WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-XL, useful for reducing bcl-XL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-XL. The oligonucleotides can be introduced into tumour cells to reduce bcl-XL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-XL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-XL production to promote the regression of vascular

Adi32132 Human CDN  
Adg65218 Human Bcl  
Aaf30926 Human Bcl  
Adg65209 Human Bcl  
Aag81698 Human thy  
Aat40079 Bcl-XL ge  
Aaz93614 Bcl-X ge  
Aas15189 Human bcl  
Aac90810 Human Bcl  
Abk84766 Human CDN  
Abt16641 Human bcl  
Add56779 Human bcl  
Ad64187 Human bcl  
Adi32104 Human CDN  
Adh52630 Human ant  
Ado19990 Human PRO  
Adp13351 Renal cel  
Aas00247 Bcl-XL-DT  
Aas00250 LFn-Bcl-X  
Adg89403 Cancer de  
Adn04260 Antipsori  
Ado19866 Human PRO  
Aax33182 Base sequ  
Adh52640 Chinese h

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-Xl mRNA

XX Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 DB 1 CTTTACTGCTGCCATGGG 18

RESULT 2  
 ABA73433  
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;  
 XX DT 01-FEB-2002 (first entry)  
 XX DE Human foetal liver single exon nucleic acid probe #21738.  
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.  
 XX PN WO200157277-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US000669.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 gene expression in human fetal liver.  
 XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.  
 XX The invention relates to a single exon nucleic acid probe for measuring  
 human gene expression in a sample derived from human foetal liver. The  
 single exon nucleic acid probes may be used for predicting, measuring and  
 displaying gene expression in samples derived from human fetal liver. The  
 present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/published\_sequences

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 DB 304 CTTTACTGCTGCCATGGG 321

RESULT 2  
 ABA73433  
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;  
 XX DT 01-FEB-2002 (first entry)  
 XX DE Human foetal liver single exon nucleic acid probe #21738.  
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.  
 XX PN WO200157277-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US000669.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

RESULT 3  
 AAI53868  
 ID AAI53868 standard; DNA; 555 BP.

XX AC AAI53868;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Probe #22554 used to measure gene expression in human placenta sample.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 gene expression in human placenta.

XX Claim 25; SEQ ID NO 22554; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
 |||||  
 DB 304 CTTTACTGCTGCCATGGG 321

RESULT 4  
 ABA38761

ID ABA38761 standard; DNA; 555 BP.

XX AC ABA38761;

XX DT 23-JAN-2002 (first entry)

XX DE Probe #17227 for gene expression analysis in human heart cell sample.

XX KW Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.



```
XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
PS
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 7
ID ABS47753 standard; DNA; 555 BP.
XX
AC ABS47753;
XX
XX 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 22743.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-48898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 22743; 659pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (i) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
```

---

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
Db 304 CTTTACTGCTGCCATGGG 321
RESULT 8
ID ABS21972 standard; DNA; 555 BP.
XX
AC ABS21972;
XX
XX 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 21963; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX ; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
```



mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pt\_sequences

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18  
|||||||  
Db 304 CTTTACTGCTGCCATGGG 321

## RESULT 9

ACH87595  
ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

DE Human; probe; ss; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.

OS Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANK/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for  
XX surveying tissues.

XX Claim 1; SEQ ID NO 20790; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and  
CC encoding at least 8 amino acids of any of the 688 amino acid sequences  
CC fully defined in the specification. The probe is a single exon probe that  
CC hybridises under high stringency conditions to a nucleic acid molecule  
CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above). The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

|||||||

Db 304 CTTTACTGCTGCCATGGG 321

## RESULT 10

ABA60917

ID ABA60917 standard; DNA; 600 BP.

XX ABA60917;

DT 01-FEB-2002 (first entry)

XX Human foetal liver: single exon nucleic acid probe #9222.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

```

PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human fetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
DB 323 CTTTACTGCTGCCATGGG 340
RESULT 11
AAI40812
ID AAI40812 standard; DNA; 600 BP.
XX
AC AAI40812;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #9498 used to measure gene expression in human placenta sample.
XX
DE Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
PF 30-JAN-2001; 2001WO-US0000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX Claim 25; SEQ ID NO 9498; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACTGCTGCCATGGG 18
DB 323 CTTTACTGCTGCCATGGG 340
RESULT 12
ABA28894
ID ABA28894 standard; DNA; 600 BP.
XX
AC ABA28894;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #7360 for gene expression analysis in human heart cell sample.
XX
DE Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
OS Homo sapiens.
XX
XX WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
PF Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 1; SEQ ID NO 7360; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic

```

```
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 13
AAK35096
ID AAK35096 standard; DNA; 600 BP.
XX
AC AAK35096;
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207458P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 14
AAK09207
```

```
ID AAK09207 standard; DNA; 600 BP.
XX
AC AAK09207;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 9198.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX
XX Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207458P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18
Db 323 CTTTACTGCTGCCATGGG 340

RESULT 15
ABS34848
ID ABS34848 standard; DNA; 600 BP.
XX
AC ABS34848;
XX
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 9838.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
OS
```

XX WO200157273-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000664.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488898/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
PS Claim 1; SEQ ID NO 9838; 658pp; English.  
XX  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTACTGCTGCCATGGG 18  
Db 323 CTTTACTGCTGCCATGGG 340  
Search completed: February 4, 2005, 21:52:42  
Job time : 232.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45, Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-6

Perfect score: 18

Sequence: 1 cttactgctgcatg99 18

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	244	2	BE818726
C 2	18	100.0	294	2	BE818722
C 3	18	100.0	310	4	BT060608
C 4	18	100.0	317	4	BT045645
C 5	18	100.0	344	8	AZ576742
C 6	18	100.0	421	4	BM844286
C 7	18	100.0	421	6	CF145335
C 8	18	100.0	456	8	AZ537061
C 9	18	100.0	474	7	CN422261
C 10	18	100.0	475	5	BQ331598
C 11	18	100.0	490	4	BG746308
C 12	18	100.0	503	4	BM857244
C 13	18	100.0	516	7	H09884
C 14	18	100.0	542	7	CN422262
C 15	18	100.0	560	6	CD675630
C 16	18	100.0	577	6	CF131978
C 17	18	100.0	584	1	AL134785
C 18	18	100.0	587	2	BE871836
C 19	18	100.0	596	2	AW732926
C 20	18	100.0	612	2	BE783664
C 21	18	100.0	619	2	BF038769
C 22	18	100.0	624	6	CF131456
C 23	18	100.0	632	7	CN422264
C 24	18	100.0	635	4	BI489889

C 25	18	100.0	648	4	BM011754
C 26	18	100.0	657	2	BE207063
C 27	18	100.0	671	2	AW814739
C 28	18	100.0	688	4	BG708652
C 29	18	100.0	697	4	BI457116
C 30	18	100.0	700	4	BG831301
C 31	18	100.0	704	4	BI561500
C 32	18	100.0	705	4	BG290422
C 33	18	100.0	711	2	BE533474
C 34	18	100.0	712	6	CD636467
C 35	18	100.0	720	6	CD636470
C 36	18	100.0	726	2	BF116000
C 37	18	100.0	731	4	BI766475
C 38	18	100.0	735	4	BI522819
C 39	18	100.0	735	6	CD641746
C 40	18	100.0	798	5	BQ687097
C 41	18	100.0	798	7	CK000319
C 42	18	100.0	818	4	BG824757
C 43	18	100.0	821	5	BQ932013
C 44	18	100.0	826	4	BG766191
C 45	18	100.0	830	7	CF619432

#### ALIGNMENTS

RESULT 1  
BE818726/c  
LOCUS BE818726 244 bp mRNA linear EST 21-SEP-2000  
DEFINITION PM3-BN0300-180700-003-c06 BN0300 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BE818726  
VERSION BE818726.1 GI:10250960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 244)  
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brundstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20204663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-pm3-BN0300-180700-003-c06&tl=2000-07-18&tl=1)  
Seq primer: puc 18 forward  
High quality sequence start: 23  
High quality sequence stop: 223.  
Location/Qualifiers  
1. 244  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BN0300"  
/note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
|||||  
DB 59 CTTTACTGCTGCCATGGG 42

## RESULT 2

BE818722/c  
LOCUS 294 bp mRNA linear EST 21-SEP-2000  
DEFINITION PM3-BN0300-080700-002-g11 BN0300 Homo sapiens cDNA, mRNA sequence.

BE818722  
ACCESSION  
VERSION BE818722.1 GI:10250956  
KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
PUBMED 20202663

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=PM3-BN0300-080

700-002-g11&t3=2000-07-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 33

High quality sequence stop: 294.

## FEATURES

source

1. .294  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BN0300"  
/note="Organ: breast normal; Vector: puc18; Site\_1: Smal;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 294;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
|||||  
DB 101 CTTTACTGCTGCCATGGG 84

## RESULT 3

BI060608  
LOCUS 310 bp mRNA linear EST 15-JUN-2001  
DEFINITION IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI060608

VERSION BI060608.1 GI:14468135

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
PUBMED 20202663

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-UT0115-

300101-433-B03&t3=2001-01-30&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 310.

## FEATURES

source

1. .310  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="UT0115"  
/note="Organ: uterus tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 310;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18  
|||||  
DB 183 CTTTACTGCTGCCATGGG 200

## RESULT 4

BI045645  
LOCUS 317 bp mRNA linear EST 14-JUN-2001  
DEFINITION MR3-FN0206-300101-004-h07 FN0206 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI045645

```

VERSION B1045645.1 GI:14452267
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., deAlvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=WR3&tl2=WR3-FN0206-
300101-004-h07&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 317.
Location/Qualifiers
FEATURES
source
1..317
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0206"
/note="Organ: prostate normal; Vector: puc18; Site 1:
SmaI; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 110 CTTTACTGCTGCCATGGG 127

RESULT 5
A2576742 344 bp DNA linear GSS 06-DEC-2000
LOCUS AST-2700919 Genetrap T47D Human Breast Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.
DEFINITION A2576742.1 GI:11563053
VERSION A2576742
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.

TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished. (2000)
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
preceded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DHS-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.
Location/Qualifiers
FEATURES
source
1..344
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
/note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA
from genetrap pools; shotgun clone in pAMP-1 and used to
transform DHS-alpha competent bacteria."
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CTTTACTGCTGCCATGGG 18
|||||
Db 185 CTTTACTGCTGCCATGGG 202

RESULT 6
BM844286/c 421 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
DEFINITION mRNA sequence.
ACCESSION BM844286
VERSION BM844286.1 GI:19200695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,H.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 63 row: B column: 03
High quality sequence stop: 421.
Location/Qualifiers
FEATURES
source
1..421
/organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S128NU216-83-B03"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"
/lab_host="Top10F"
/clone_lib="S128NU216"
/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

```

## ORIGIN

```

Query Match      100.0%; Score 18; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CTTTACTGCTGCCATGGG 18
        |||||
Db      264 CTTTACTGCTGCCATGGG 247

```

## RESULT 7

```

CF145335/c
LOCUS      CF145335      421 bp      mRNA      linear      EST 06-AUG-2003
DEFINITION      UI-HF-C80-asn-f-06-0-UI-r1 NIH_MGC_210 Homo sapiens cDNA clone
IMAGE:30569057 5', mRNA sequence.
ACCESSION      CF145335
VERSION        CF145335.1 GI:33260779
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477
PUBMED      8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratliff
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.

```

## FEATURES

```

source
1..421
/mol_type="mRNA"
/organism="Homo sapiens"

```

```

/db_xref="taxon:9606"
/clone="IMAGE:30569057"
/tissue_type="CNCAP(3)T-225 cell line"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC 210"
/notes="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size sorted according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CTTTACTGCTGCCATGGG 18
        |||||
Db      258 CTTTACTGCTGCCATGGG 241

```

## RESULT 8

```

AZ537061
LOCUS      AZ537061      456 bp      DNA      linear      GSS 06-NOV-2000
DEFINITION      AST-2P01514.AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.
ACCESSION      AZ537061
VERSION        AZ537061.1 GI:11113828
KEYWORDS      GSS.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a PC-3 GenomesScreen(TM) Library
Unpublished (2000)
Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomesScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.

```

## FEATURES

```

source
1..456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
Library"
/notes="Organ: Prostate; Vector: pAmp-1; 3' RACE of total

```



RNA from genetrapp pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

## ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

Db 436 CTTTACTGCTGCCATGGG 453

## RESULT 9

CN422261/c  
LOCUS CN422261 474 bp mRNA linear EST 16-MAY-2004  
DEFINITION 1700424524125 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN422261

VERSION CN422261.1 GI:47409855

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 474 Std Error: 0.00.

## FEATURES

## source

1..474

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cells, embryoid bodies

derived from H1, H7 and H9 cells"

/clone\_lib="GRN\_EB"

/note="oligo dT primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from HES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 474;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

Db 319 CTTTACTGCTGCCATGGG 302

## RESULT 10

BQ331598/c  
LOCUS BQ331598 475 bp mRNA linear EST 17-MAY-2002  
DEFINITION MR4-ET0138-080501-010-006 ET0138 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ331598

VERSION BQ331598.1 GI:20972765

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 475)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

## COMMENT

Contact: Simpson A.J.J.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ET0138-080501-010-006&t3=2001-05-08&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 41

High quality sequence stop: 475.

## FEATURES

## source

1..475

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev stage="Adult"

/clone\_lib="ET0138"

/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (O.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 475;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTGCCATGGG 18

Db 153 CTTTACTGCTGCCATGGG 136

## RESULT 11

## LOCUS

BG746308/c  
602703549F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4856725 5',  
mRNA sequence.

BG746308

BG746308.1 GI:14056961

EST.

SOURCE Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: csapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI708 row: a column: 14  
 High quality sequence stop: 464.

# FEATURES

```

source
1. 490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4856725"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/notes="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 399 CTTTACTGCTGCCATGGG 382

RESULT 12
BM857244/c
LOCUS
DEFINITION K-EST0141477 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-78-F09 5',
mRNA sequence.
ACCESSION BM857244
VERSION BM857244.1 GI:19213643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 78 row: F column: 09
High quality sequence stop: 503.
Location/Qualifiers
1. 503
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNUS20-78-F09"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/clone_lib="S21SNUS20"

```

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F' by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

# ORIGIN

```

Query Match 100.0%; Score 18; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGCTGCCATGGG 18
|||||
Db 265 CTTTACTGCTGCCATGGG 248

RESULT 13
H09884/c
LOCUS
DEFINITION H09884 516 bp mRNA linear EST 23-JUN-1995
IMAGE:46778 5' similar to SP:A47537 APOPTOSIS REGULATOR
ECL-X - ; mRNA sequence.
ACCESSION H09884
VERSION H09884.1 GI:874706
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterson,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wuston.wustl.edu
Insert Size: 1997
High quality sequence stops: 249
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1997 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 249.
Location/Qualifiers
1. 516
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:419319"
/db_xref="taxon:9606"
/clone="IMAGE:46778"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain 1N1B"

```

# FEATURES

```

source
1. 516
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:419319"
/db_xref="taxon:9606"
/clone="IMAGE:46778"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain 1N1B"

```

/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGAAATTCGCGCCGACGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lfamid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 516;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTCCCATGGG 18  
|||||  
Db 78 CTTTACTGCTCCCATGGG 61

RESULT 14  
CN422262/c  
LOCUS  
DEFINITION 17000424524143 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN422262  
VERSION CN422262.1 GI:47409856  
KEYWORDS EST.  
SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 542)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,  
Lebkowski, J. and Stanton, L. W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 542 Std Error: 0.00.

## FEATURES

source

Location/Qualifiers  
1..542

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_lib="GRN\_EB"  
/note="oligo dr primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from HES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 542;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTCCCATGGG 18  
|||||  
Db 327 CTTTACTGCTCCCATGGG 310

RESULT 15  
CD675630/c  
LOCUS  
DEFINITION fs25h07.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone

fs25h07 5', mRNA sequence.

CD675630

CD675630.1 GI:32177361

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 560)  
Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of adult human lens for the NEIBank  
Project: over 2000 non-redundant transcripts, novel genes and  
splice variants  
Mol. Vis. 8 (4), 171-184 (2002)  
22103463  
12107413

COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 25 row: h column: 07

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1..560

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="fs25h07"

/tissue type="Adult"

/dev stage="Adult"

/lab\_host="EMDH10B"

/clone\_lib="Human Lens cDNA (Normalized): fs"

/note="Organ: Eye; Vector: pCMVSPORT6; A human lens  
library (by) was normalized by self-subtraction. One  
portion of double stranded plasmid DNA representing the  
library was linearized by NotI. This NotI digested library  
was used as a template for biotinylated RNA synthesis  
using SP6 RNA polymerase. Another portion of the double  
stranded plasmid library was converted to single-stranded  
circles in vitro using Gene II and Exonuclease III (Life  
Technologies). Single-stranded DNA (1 mg) was hybridized  
(Cot 500) with 41 mg of Bio-RNA and vector blocking  
oligonucleotides. The hybridized Bio-RNA/ss-circles were  
removed by streptavidin:phenol extraction. EST analysis  
was performed on the library at the NIH Intramural  
Sequencing Center(NISC)."

Query Match 100.0%; Score 18; DB 6; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTACTGCTCCCATGGG 18  
|||||  
Db 490 CTTTACTGCTCCCATGGG 473

Search completed: February 5, 2005, 08:11:44  
Job time : 2148.2 secs

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 480.738 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-7  
Perfect score: 20  
Sequence: 1 cgcggtctctggtatccaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD235155
2	20	100.0	20	6	BD235171
3	20	100.0	541	4	AF245487
4	20	100.0	541	4	AF245488
5	20	100.0	541	4	AF245489
6	20	100.0	555	6	CQ113695
7	20	100.0	555	6	CQ125274
8	20	100.0	555	6	CQ185831
9	20	100.0	555	6	CQ235904
10	20	100.0	555	6	CQ273477
11	20	100.0	555	6	CQ310858
12	20	100.0	555	6	CQ347773
13	20	100.0	600	6	CQ100639
14	20	100.0	600	6	CQ139631
15	20	100.0	600	6	CQ175964
16	20	100.0	600	6	CQ223999
17	20	100.0	600	6	CQ260961
18	20	100.0	600	6	CQ298444
19	20	100.0	600	6	CQ335104

C 20	20	100.0	636	6	BD097037
C 21	20	100.0	695	6	AX525912
C 22	20	100.0	699	10	MMBC1XL
C 23	20	100.0	702	6	BD084108
C 24	20	100.0	702	6	BD102202
C 25	20	100.0	702	9	BT007208
C 26	20	100.0	702	10	MMU10101
C 27	20	100.0	702	12	BT008248
C 28	20	100.0	720	4	AF216205
C 29	20	100.0	723	9	HSU72398
C 30	20	100.0	726	10	RNU34963
C 31	20	100.0	726	10	S76513
C 32	20	100.0	747	6	AX127722
C 33	20	100.0	752	4	SSJ001203
C 34	20	100.0	764	10	RNU10579
C 35	20	100.0	765	4	AF164517
C 36	20	100.0	926	6	AR054021
C 37	20	100.0	926	6	AR118504
C 38	20	100.0	926	6	AR124952
C 39	20	100.0	926	6	AR144311
C 40	20	100.0	926	6	AR172594
C 41	20	100.0	926	6	BD243042
C 42	20	100.0	926	6	CQ765842
C 43	20	100.0	926	6	E58777
C 44	20	100.0	926	6	I52011
C 45	20	100.0	926	6	AR371661

ALIGNMENTS

RESULT 1  
LOCUS BD235155 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xl.  
ACCESSION BD235155  
VERSION BD235155.1 GI:33044925  
KEYWORDS JP 2002519048-A/7.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Stein,C.A.  
TITLE Oligonucleotide inhibitors of bcl-xl  
JOURNAL Patent: JP 2002519048-A 7 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/7  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PI 02-JUL-1998 US 09/109614  
CY A STEIN

PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..20  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGCGTTCCTCTGATCCAA 20  
|||||



/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="1.2"  
<1..>541  
/codon\_start=1  
/product="anti-apoptotic regulator Bcl-xL"  
/protein\_id="AAK31307.1"  
/db\_xref="GI:13591638"  
/translation="INGNPSWHLADSPAVNGATGHSRSDAREVIPMAAVKQALREAG  
DEFELRRAPSDTSLQHIPTGTAYOSFEQVNVLEFRDGVNMGRIIVAFPSFGGALCV  
ESVDKEMQVLRSIATWMTYINDHLEPFIQENGWDTFVELYGNNAASRSKQGERF  
NRWELTGMTAGVVLGSLF"

## CDS

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20  
|||||  
Db 409 CGCGTTCTCTCGATCCAA 390

## RESULT 5

AF245489/c  
LOCUS AF245489 541 bp mRNA linear MAM 11-APR-2001  
DEFINITION Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.  
ACCESSION AF245489  
VERSION AF245489.1 GI:13591639  
KEYWORDS  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (Bases 1 to 541)  
Amills, M. and Bouzat, J.  
TITLE Characterization of the bovine bcl-xL gene and related pseudogenes  
JOURNAL Unpublished  
REFERENCE 2 (Bases 1 to 541)  
Amills, M. and Bouzat, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autònoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

## FEATURES

Location/Qualifiers  
1..541  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="1.3"  
<1..>541  
/codon\_start=1  
/product="anti-apoptotic regulator Bcl-xL"  
/protein\_id="AAK31308.1"  
/db\_xref="GI:13591640"  
/translation="INGNPSWHLADSPAVNGATGHSRSDAREVIPMAAVKQALREAG  
DEFELRRAPSDTSLQHIPTGTAYOSFEQVNVLEFRDGVNMGRIIVAFPSFGGALCV  
ESVDKEMQVLRSIATWMTYINDHLEPFIQENGWDTFVELYGNNAASRSKQGERF  
NRWELTGMTAGVVLGSLF"

## CDS

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20  
|||||  
Db 409 CGCGTTCTCTCGATCCAA 390

RESULT 6  
CQ113695  
LOCUS CQ113695 555 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 22554 from Patent WO0157272.  
ACCESSION CQ113695  
VERSION CQ113695.1 GI:41083565  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 22554 09-AUG-2001;  
Aescmica, Inc. (US)  
FEATURES  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA. SIGNAL = 0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST.HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20  
|||||  
Db 6 CGCGTTCTCTCGATCCAA 25

## RESULT 7

CQ152574  
LOCUS CQ152574 555 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 22596 from Patent WO0157276.  
ACCESSION CQ152574  
VERSION CQ152574.1 GI:41159924  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 22596 09-AUG-2001;  
Aescmica, Inc. (US)  
FEATURES  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW. SIGNAL = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST.HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00"

Qy 1 CGCGTTCTCTCGATCCAA 20  
|||||  
Db 6 CGCGTTCTCTCGATCCAA 25

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTCGATCCAA 20  
|||||  
Db 6 CGCGTTCTCTCGATCCAA 25

```

RESULT 8
LOCUS      CQ185831
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION  CQ185831
VERSION     CQ185831.1 GI:41180846
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL     Patent: WO 0157274-A 17227 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
            1.4-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN HIT:
            BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCGTTCTCTCGATCCAA 20
        |||||
Db      6 CGCCGTTCTCTCGATCCAA 25

RESULT 9
LOCUS      CQ235904
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION  CQ235904
VERSION     CQ235904.1 GI:41219192
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
            ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
            3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
            60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
            August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
            (03.10.00)<150> US 60/236,359<151> 27 September 2000
            (27.09.00)<150> US 60/234,687<151> 21 September 2000
            (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
            Molecular Dynamics Sequence Listing Engine
            Patent: WO 0157273-A 22743 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL =
            1.7-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"

ORIGIN

```

```

Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCGTTCTCTCGATCCAA 20
        |||||
Db      6 CGCCGTTCTCTCGATCCAA 25

RESULT 10
LOCUS      CQ273477
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION  CQ273477
VERSION     CQ273477.1 GI:41246081
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human fetal liver
JOURNAL     Patent: WO 0157277-A 21738 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
            = 3.5-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN
            HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGCCGTTCTCTCGATCCAA 20
        |||||
Db      6 CGCCGTTCTCTCGATCCAA 25

RESULT 11
LOCUS      CQ310858
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION     CQ310858.1 GI:41271435
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 21963 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
            2-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST_HUMAN HIT:
            BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE
            0.00e+00"

ORIGIN

```



Query Match 100.0%; Score 20; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 6 CGCGTTCTCTGGATCCAA 25

RESULT 12  
CQ347773  
LOCUS CQ347773 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21867 from Patent WO0157275.  
ACCESSION CQ347773  
VERSION CQ347773.1 GI:41296844  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;  
Acemica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =  
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 6 CGCGTTCTCTGGATCCAA 25

RESULT 13  
CQ100639  
LOCUS CQ100639 600 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 9498 from Patent WO0157272.  
ACCESSION CQ100639  
VERSION CQ100639.1 GI:41069665  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 9498 09-AUG-2001;  
Acemica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..600  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =  
0.99"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 25 CGCGTTCTCTGGATCCAA 44

RESULT 14  
CQ139631  
LOCUS CQ139631 600 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 9653 from Patent WO0157276.  
ACCESSION CQ139631  
VERSION CQ139631.1 GI:41097003  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 9653 09-AUG-2001;  
Acemica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..600  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL  
= 4.7"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 25 CGCGTTCTCTGGATCCAA 44

RESULT 15  
CQ175964  
LOCUS CQ175964 600 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 7360 from Patent WO0157274.  
ACCESSION CQ175964  
VERSION CQ175964.1 GI:41170703  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human heart  
JOURNAL Patent: WO 0157274-A 7360 09-AUG-2001;  
Acemica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..600  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 600;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-7  
Perfect score: 20  
Sequence: 1 cgcgcgtctctggtaccaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	20	100.0	20	3	AAZ46977
2	20	100.0	337	10	ADK66037
3	20	100.0	492	9	ACH46093
4	20	100.0	555	4	ABA73433
5	20	100.0	555	4	AAI53868
6	20	100.0	555	4	ABA38761
7	20	100.0	555	4	AAK48039
8	20	100.0	555	4	AAK21876
9	20	100.0	555	4	ABS47753
10	20	100.0	555	6	ABS21972
11	20	100.0	564	12	ACH87595
12	20	100.0	600	4	ABA60917
13	20	100.0	600	4	AAI40812
14	20	100.0	600	4	ABA28894
15	20	100.0	600	4	AAK35096
16	20	100.0	600	4	AAK09207
17	20	100.0	600	4	ABS34848
18	20	100.0	600	6	ABS09558
19	20	100.0	636	4	AAH48169
20	20	100.0	695	6	ABT09346
21	20	100.0	702	5	AAH43464

C 22	20	100.0	702	12	ADM45994
C 23	20	100.0	739	12	ADG65218
C 24	20	100.0	747	4	AAF30926
C 25	20	100.0	747	12	ADG65209
C 26	20	100.0	926	2	AAQ81698
C 27	20	100.0	926	2	AAQ40079
C 28	20	100.0	926	3	AAZ93614
C 29	20	100.0	926	4	AAAS15189
C 30	20	100.0	926	4	AAC90810
C 31	20	100.0	926	6	ABK84766
C 32	20	100.0	926	8	ABT16641
C 33	20	100.0	926	10	ADD56779
C 34	20	100.0	926	10	AAE64187
C 35	20	100.0	926	11	ADI32104
C 36	20	100.0	926	12	ADH52630
C 37	20	100.0	926	12	ADQ19990
C 38	20	100.0	926	12	ADP13351
C 39	20	100.0	1236	5	AAAS00247
C 40	20	100.0	1384	2	AAV17638
C 41	20	100.0	1455	5	AAAS00250
C 42	20	100.0	1466	10	AD885177
C 43	20	100.0	1742	4	AAF75960
C 44	20	100.0	1748	10	ADB58615
C 45	20	100.0	1748	10	ADB53263

ALIGNMENTS

RESULT 1  
AAZ46977  
ID AAZ46977 standard; DNA; 20 BP.  
XX  
AC AAZ46977;  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-Xl mRNA specific antisense oligo G.  
XX  
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Stein CA;  
XX  
DR WPI; 2000-137140/12.  
XX  
PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
XX  
PS Claim 1; Fig 1; 69pp; English.  
XX  
CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
CC pharmaceutical compositions, useful as above. Sequences AA246971-983  
CC represent antisense oligos specific for the bcl-Xl mRNA  
XX

SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTGGATCCAA 20  
|||||  
DB 1 CGCGGTTCTCTGGATCCAA 20  
|||||

RESULT 2  
ADK66037/c  
ID ADK66037 standard; DNA; 337 BP.  
XX AC ADK66037;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Standardized polynucleotide system polynucleotide #8.  
XX  
XX ss; standardized polynucleotide system; medical diagnosis;  
KW functional genomics; sample analysis; pharmacogenomics; sample analysis.  
XX  
XX Unidentified.  
XX  
XX DE10209071-Al.  
XX  
XX 25-SEP-2003.  
XX  
XX 28-FEB-2002; 2002DE-01009071.  
XX  
XX 28-FEB-2002; 2002DE-01009071.  
XX  
XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
XX  
XX Koehler T, Rost A;  
XX  
XX WPI; 2003-732912/70.  
XX

PT Standardized polynucleotide system, useful for quantitative, real-time  
PT determination of nucleic acid, comprises stabilized standards, primers  
PT and probe.  
XX  
XX Claim 1; Page 7; 38pp; German.  
XX

CC The present invention relates to a standardized polynucleotide system,  
CC which comprises at least one carrier nucleic acid, at least 3  
CC oligonucleotides, as primers and target-specific, fluorescently labeled  
CC probe and optionally at least one set of stabilized controls (standard  
CC RNA or DNA) of known concentration and instructions. The system comprises  
CC any of 20 sets of one control, two primers and one target-specific probe.  
CC The standardized polynucleotide system can be used for quantitative, real  
CC -time detection of target nucleic acids, especially analysis of genes or  
CC gene products, e.g. for individualized medical diagnosis, in veterinary  
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
CC pharmaceutical testing, analysis of food or environmental samples and  
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present  
CC sequence is a polynucleotide used in the system of the invention.  
XX  
XX SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTGGATCCAA 20  
|||||

DB 156 CGCGGTTCTCTGGATCCAA 137

RESULT 3  
ACH46093/c  
ID ACH46093 standard; cDNA; 492 BP.  
XX ACH46093;  
XX

DT 13-OCT-2003 (first entry)  
XX  
XX Human infant brain cDNA #156.  
XX

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.  
XX

OS Homo sapiens.  
XX  
XX US2003073623-Al.  
XX

PD 17-APR-2003.  
XX

PF 30-JUL-2001; 2001US-00918995.  
XX

PR 30-JUL-2001; 2001US-00918995.  
XX

PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
XX

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX

DR WPI; 2003-615964/58.  
XX

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX

PS Claim 1; SEQ ID NO 33305; 44pp; English.  
XX

CC The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
XX

SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 492;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGTTCTCTGGATCCAA 20  
|||||

DB 340 CGCGGTTCTCTGGATCCAA 321  
|||||

RESULT 4

```

ABA73433
ID ABA73433 standard; DNA; 555 BP.
XX
AC ABA73433;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #21738.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PF WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCAA 20
Db 6 CGCGTTCTCTGGATCAA 25

RESULT 5
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX
AC AAI53868;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #22554 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCAA 20
Db 6 CGCGTTCTCTGGATCAA 25

RESULT 5
AAI53868
ID AAI53868 standard; DNA; 555 BP.
XX
AC AAI53868;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #17227 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
XX
KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PF WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 22554; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCAA 20
Db 6 CGCGTTCTCTGGATCAA 25

RESULT 6
ABA38761
ID ABA38761 standard; DNA; 555 BP.
XX
AC ABA38761;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #17227 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
XX
KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX

```



RESULT 10

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 555;

Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20

Db 6 CGCCGTTCTCTCGATCCAA 25

# RESULT 11

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

AC ACH87595;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

DE Human; probe; ss; gene expression; single exon probe; microarray;

XX alternative splicing event; genomic alteration.

KW Homo sapiens.

XX US2003194704-A1.

PN 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

PF 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

PI WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 1; SEQ ID NO 20790; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridizes under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX SQ Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20

Db 6 CGCCGTTCTCTCGATCCAA 25

# RESULT 12

ABA60917

ID ABA60917 standard; DNA; 600 BP.

XX ABA60917;

AC ABA60917;

DT 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #9222.

DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

OS WO200157277-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.



CC The present invention relates to single exon nucleic acid probes (SENPs).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders  
 xx  
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 20; DB 4; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

AC AAK35096;  
XX  
DT  
XX 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157276-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000668.  
PF  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GE-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488900/53.  
DR  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX  
XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.  
PS  
XX  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention  
XX  
XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGCGGTTCCTCGATCCAA 20  
Db 25 CGCGGTTCCTCGATCCAA 44

Search completed: February 4, 2005, 21:52:42  
Job time : 258.033 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2384.67 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-7  
Perfect score: 20  
Sequence: 1 cgcggtctctggtatccaa 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsl1:\*

9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	101	9	CL569679
C 2	20	100.0	107	9	CL569678
C 3	20	100.0	119	9	CL569637
C 4	20	100.0	119	9	CL569651
C 5	20	100.0	119	9	CL569677
C 6	20	100.0	119	9	CL569687
C 7	20	100.0	119	9	CL569770
C 8	20	100.0	119	9	CL569771
C 9	20	100.0	119	9	CL569805
C 10	20	100.0	119	9	CL569908
C 11	20	100.0	119	9	CL569911
C 12	20	100.0	119	9	CL570137
C 13	20	100.0	125	9	CL570142
C 14	20	100.0	125	9	CL569466
C 15	20	100.0	126	9	CL569669
C 16	20	100.0	126	9	CL569866
C 17	20	100.0	126	9	CL569869
C 18	20	100.0	126	9	CL569905
C 19	20	100.0	126	9	CL569975
C 20	20	100.0	126	9	CL569987
C 21	20	100.0	126	9	CL570033
C 22	20	100.0	127	9	CL569665
C 23	20	100.0	127	9	CL569672
C 24	20	100.0	127	9	CL569673

C 25 20 100.0 129 9 CL569909

C 26 20 100.0 132 9 CL569680

C 27 20 100.0 135 9 CL570034

C 28 20 100.0 165 9 CL569907

C 29 20 100.0 198 9 CL569873

C 30 20 100.0 201 9 CL569868

C 31 20 100.0 207 9 CL569540

C 32 20 100.0 211 9 CL569804

C 33 20 100.0 212 9 CL569870

C 34 20 100.0 212 9 CL569904

C 35 20 100.0 216 2 BF806802

C 36 20 100.0 231 4 BM818607

C 37 20 100.0 232 2 BF804861

C 38 20 100.0 251 9 CL569871

C 39 20 100.0 280 9 CL569872

C 40 20 100.0 283 2 BF823588

C 41 20 100.0 298 9 CL569565

C 42 20 100.0 299 7 F08773

C 43 20 100.0 305 4 BI399503

C 44 20 100.0 332 2 AW820481

C 45 20 100.0 356 2 AW244806

#### ALIGNMENTS

RESULT 1

LOCUS CL569679/c

DEFINITION AQ0730 Sanger Institute Gene Trap Library pGT01xr Mus musculus

ACCESSION CL569679

VERSION CL569679.2 GI:48774271

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

101 bp mRNA linear GSS 16-JUN-2004

CDNA, mRNA sequence.

CL569679

CL569679.2 GI:48774271

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Sanger Institute Gene Trap Resource - SIGTR.

http://www.sanger.ac.uk/PostGenomics/genetrap/

Unpublished (2003)

On Jun 16, 2004 this sequence version replaced gi:48375778.

Contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: info.genetrap@sanger.ac.uk

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from Sanger Institute Gene Trap

Resource. Annotation information available from

http://www.sanger.ac.uk/PostGenomics/genetrap/

Class: Gene Trap.

Location/Qualifiers

1. .101

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129 OLA"

/db\_xref="taxon:10090"

/sex="Male"

/cell\_type="Embryonic Stem Cell"

/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"

/note="Vector: pGT01xr"

#### ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 101;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGCGGTTCTCTCGGATCCAA 20

|||||

91 CGCGGTTCTCTCGGATCCAA 72

```

RESULT 2
LOCUS      CL569678/c
DEFINITION 107 bp mRNA linear GSS 16-JUN-2004
cdNA, mRNA sequence.
ACCESSION  CL569678
VERSION     CL569678.2 GI:48774270
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 107)
AUTHORS   Sanger Institute Gene Trap Library pGT01xr Mus musculus
TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL   Unpublished (2003)
COMMENT   On Jun 16, 2004 this sequence version replaced gi:48375777.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES             Location/Qualifiers
     source          1..107
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 102 CGCCGTTCTCTCGATCCAA 83

FEATURES             Location/Qualifiers
     source          1..107
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 102 CGCCGTTCTCTCGATCCAA 83

RESULT 3
LOCUS      CL569637/c
DEFINITION 119 bp mRNA linear GSS 16-JUN-2004
cdNA, mRNA sequence.
ACCESSION  CL569637
VERSION     CL569637.2 GI:48774229
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 119)
AUTHORS   Sanger Institute Gene Trap Library pGT01xr Mus musculus
TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL   Unpublished (2003)
COMMENT   On Jun 16, 2004 this sequence version replaced gi:48375736.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES             Location/Qualifiers
     source          1..119
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 114 CGCCGTTCTCTCGATCCAA 95

FEATURES             Location/Qualifiers
     source          1..119
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 4
LOCUS      CL569651/c
DEFINITION 119 bp mRNA linear GSS 16-JUN-2004
cdNA, mRNA sequence.
ACCESSION  CL569651
VERSION     CL569651.2 GI:48774243
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 119)
AUTHORS   Sanger Institute Gene Trap Library pGT01xr Mus musculus
TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL   Unpublished (2003)
COMMENT   On Jun 16, 2004 this sequence version replaced gi:48375750.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES             Location/Qualifiers
     source          1..119
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 5
LOCUS      CL569677/c
DEFINITION 119 bp mRNA linear GSS 16-JUN-2004
cdNA, mRNA sequence.
ACCESSION  CL569677
VERSION     CL569677.2 GI:48774270
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 119)
AUTHORS   Sanger Institute Gene Trap Library pGT01xr Mus musculus
TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL   Unpublished (2003)
COMMENT   On Jun 16, 2004 this sequence version replaced gi:48375736.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES             Location/Qualifiers
     source          1..119
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 6
LOCUS      CL569677/c
DEFINITION 119 bp mRNA linear GSS 16-JUN-2004
cdNA, mRNA sequence.
ACCESSION  CL569677
VERSION     CL569677.2 GI:48774270
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 119)
AUTHORS   Sanger Institute Gene Trap Library pGT01xr Mus musculus
TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL   Unpublished (2003)
COMMENT   On Jun 16, 2004 this sequence version replaced gi:48375736.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.

FEATURES             Location/Qualifiers
     source          1..119
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT01xr"
                     /note="Vector: pGT01xr"

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20
Db 114 CGCCGTTCTCTCGATCCAA 95

```

[illegible]

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)  
Sanger Institute Gene Trap Resource - SIGTR.  
http://www.sanger.ac.uk/PostGenomics/genetrap/  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48375870.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetrap@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetrap/  
Class: Gene Trap.

FEATURES  
source  
1. .119  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20  
|||||  
Db 114 CGCCGTTCTCTCGATCCAA 95

RESULT 9  
CL569805/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CL569805 119 bp mRNA linear GSS 16-JUN-2004  
AR0493 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
cDNA, mRNA sequence.  
CL569805  
CL569805.2 GI:48774397  
GSS.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)  
Sanger Institute Gene Trap Resource - SIGTR.  
http://www.sanger.ac.uk/PostGenomics/genetrap/  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48375904.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetrap@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetrap/  
Class: Gene Trap.

FEATURES  
source  
1. .119  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGTTCTCTCGATCCAA 20  
|||||  
Db 114 CGCCGTTCTCTCGATCCAA 95

## RESULT 10

## CL569908/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## CL569908

## AR1185 Sanger Institute Gene Trap Library pGT01xr Mus musculus

## cDNA, mRNA sequence.

## CL569908

## CL569908.2 GI:48774500

## GSS.

## Mus musculus (house mouse)

## Mus musculus

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 119)

## Sanger Institute Gene Trap Resource - SIGTR.

## http://www.sanger.ac.uk/PostGenomics/genetrap/

## Unpublished (2003)

## On Jun 16, 2004 this sequence version replaced gi:48376007.

## Contact: Sanger Institute Gene Trap Resource - SIGTR

## Wellcome Trust Sanger Institute

## Email: info.genetrap@sanger.ac.uk

## Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from

## http://www.sanger.ac.uk/PostGenomics/genetrap/

## Class: Gene Trap.

## Location/Qualifiers

## 1. .119

## /organism="Mus musculus"

## /mol\_type="mRNA"

## /strain="129 OLA"

## /db\_xref="taxon:10090"

## /sex="Male"

## /cell\_type="Embryonic Stem Cell"

## /clone\_lib="Sanger Institute Gene Trap Library pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

## /note="Vector: pGT01xr"

JOURNAL  
COMMENT  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48376010.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetraps@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from Sanger Institute Gene Trap  
Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Class: Gene Trap.

FEATURES  
source  
Location/Qualifiers  
1..119  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 12  
CL570137/c  
LOCUS  
DEFINITION AV0131 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
CDNA, mRNA sequence.

ACCESSION CL570137  
VERSION CL570137.2 GI:48774729  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 119)  
Sanger Institute Gene Trap Resource - SIGTR.  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48376236.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetraps@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from Sanger Institute Gene Trap  
Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Class: Gene Trap.

FEATURES  
source  
Location/Qualifiers  
1..119  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 114 CGCGTTCTCTGGATCCAA 95

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 13  
CL570142/c  
LOCUS  
DEFINITION AV0189 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
CDNA, mRNA sequence.

ACCESSION CL570142  
VERSION CL570142.2 GI:48774734  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 119)  
Sanger Institute Gene Trap Resource - SIGTR.  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48376241.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetraps@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from Sanger Institute Gene Trap  
Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Class: Gene Trap.

FEATURES  
source  
Location/Qualifiers  
1..119  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGTTCTCTGGATCCAA 20  
|||||  
Db 114 CGCGTTCTCTGGATCCAA 95

RESULT 14  
CL569466/c  
LOCUS  
DEFINITION AN0071 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
CDNA, mRNA sequence.

ACCESSION CL569466  
VERSION CL569466.2 GI:48774058  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 125)  
Sanger Institute Gene Trap Resource - SIGTR.  
http://www.sanger.ac.uk/PostGenomics/genetraps/  
Unpublished (2003)  
On Jun 16, 2004 this sequence version replaced gi:48375565.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetraps@sanger.ac.uk

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetrap/>  
Class: Gene Trap.

FEATURES  
source

1..125  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 125;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGCCGTTCTCTGGATCCAA 20  
|||||  
Db 120 CGCCGTTCTCTGGATCCAA 101

RESULT 15  
CL569669/c

LOCUS 126 bp mRNA linear GSS 16-JUN-2004  
DEFINITION AQ0663 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
CDNA, mRNA sequence.  
ACCESSION CL569669  
VERSION CL569669.2 GI:48774261  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 126)  
Sanger Institute Gene Trap Resource - SIGTR.  
TITLE <http://www.sanger.ac.uk/PostGenomics/genetrap/>  
JOURNAL Unpublished (2003)  
COMMENT On Jun 16, 2004 this sequence version replaced gi:48375768.  
Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: [info.genetrap@sanger.ac.uk](mailto:info.genetrap@sanger.ac.uk)  
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from <http://www.sanger.ac.uk/PostGenomics/genetrap/>  
Class: Gene Trap.

FEATURES  
source

1..126  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 126;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGCCGTTCTCTGGATCCAA 20  
|||||  
Db 121 CGCCGTTCTCTGGATCCAA 102



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-8  
Perfect score: 18  
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235156
2	18	100.0	18	6	BD235173
3	18	100.0	18	6	BD235174
4	18	100.0	65	6	CQ559048
5	18	100.0	512	6	CQ727769
6	18	100.0	513	10	MMUL10100
7	18	100.0	513	10	AF136230
8	18	100.0	513	10	AF279286
9	18	100.0	537	10	S78284
10	18	100.0	555	6	CQ113695
11	18	100.0	555	6	CQ152574
12	18	100.0	555	6	CQ185831
13	18	100.0	555	6	CQ235904
14	18	100.0	555	6	CQ273477
15	18	100.0	555	6	CQ310858
16	18	100.0	555	6	CQ347773
17	18	100.0	600	6	CQ106639
18	18	100.0	600	6	CQ139631
19	18	100.0	600	6	CQ175964

20	18	100.0	600	6	CQ222999	Sequence
21	18	100.0	600	6	CQ260961	Sequence
22	18	100.0	600	6	CQ298444	Sequence
23	18	100.0	600	6	CQ335104	Sequence
c 24	18	100.0	600	6	AX925692	Sequence
c 25	18	100.0	660	6	AX925694	Sequence
c 26	18	100.0	660	6	AX925696	Sequence
c 27	18	100.0	695	6	AX525912	Sequence
c 28	18	100.0	699	10	MMBCLXL	Sequence
c 29	18	100.0	702	4	AY005131	Sequence
c 30	18	100.0	702	6	BD084108	Method of
c 31	18	100.0	702	6	BD102202	Method fo
c 32	18	100.0	702	9	BT007208	Homo sapi
c 33	18	100.0	702	10	MMUL10101	Mus musculu
c 34	18	100.0	702	12	BT008248	Synthetic
c 35	18	100.0	720	4	AF216205	Sus scrofa
c 36	18	100.0	723	9	HSU72398	Human Bcl-x
c 37	18	100.0	726	10	RNU34963	Rattus norv
c 38	18	100.0	726	10	S76513	Bcl-x=apopt
c 39	18	100.0	737	6	AR054022	Sequence
c 40	18	100.0	737	6	AR172595	Sequence
c 41	18	100.0	737	6	I52012	Sequence
c 42	18	100.0	737	6	AR371662	Sequence
c 43	18	100.0	737	6	AR380913	Sequence
c 44	18	100.0	737	9	HSBCLXS	H. sapiens b
c 45	18	100.0	747	6	AX127722	Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS BD235156 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xl.  
ACCESSION BD235156  
VERSION BD235156.1 GI:33044926  
KEYWORDS JP 2002519048-A/8.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xl  
JOURNAL Patent: JP 2002519048-A 8 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/8  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PI 02-JUL-1998 US 09/109614  
CY A STEIN

PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC  
A61K47/42,  
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

#### ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||||

Db 1 CTGACTCCAGCTGTATCC 18

RESULT 2  
BD235173  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD235173 18 bp DNA linear PAT 17-JUL-2003  
Oligonucleotide inhibitors of bcl-xL.  
BD235173  
BD235173.1 GI:33044943  
JP 2002519048-A/25.  
synthetic construct  
artificial sequences.  
1 (bases 1 to 18)  
Stein, C.A.  
Oligonucleotide inhibitors of bcl-xL  
Patent: JP 2002519048-A 25 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
OS Artificial Sequence  
PN JP 2002519048-A/25  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC

C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC  
A61K47/42,  
A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc\_binding (1)..(4)  
FT misc\_binding (5)..(8)  
FT misc\_binding (11)..(12)  
FT misc\_binding (15)..(18).

FEATURES  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 1 CTGACTCCAGCTGTATCC 18

RESULT 4  
CQ559048/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CQ559048 65 bp DNA linear PAT 30-JAN-2004  
Sequence 28683 from Patent WO0210449.  
CQ559048  
CQ559048.1 GI:41525475  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
Patent: WO 0210449-A 28683 07-FEB-2002;  
Compugen Inc. (US)  
Location/Qualifiers  
1..65  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"

FEATURES  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 1 CTGACTCCAGCTGTATCC 18

/db\_xref="taxon:10090"

# ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 65;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 31 CTGACTCCAGCTGTATCC 14

## RESULT 5

LOCUS CQ727769/c 512 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 13703 from Patent WO02068579.  
ACCESSION CQ727769  
VERSION CQ727769.1 GI:42294740

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof

JOURNAL Patent: WO 02068579-A 13703 06-SEP-2002;  
PE Corporation (NY) (US)

## FEATURES

source  
1..512  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

# ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 512;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 212 CTGACTCCAGCTGTATCC 195

## RESULT 6

LOCUS MMU10100/c 513 bp mRNA linear ROD 30-NOV-1995  
DEFINITION Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.  
ACCESSION U10100  
VERSION U10100.1 GI:506645

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 513)

AUTHORS Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W.  
TITLE Cloning and molecular characterization of mouse bcl-x in B and T  
lymphocytes

JOURNAL J. Immunol. 153 (10), 4388-4398 (1994)

MEDLINE 95052604  
PUBMED 7963517

REFERENCE 2 (bases 1 to 513)

AUTHORS Behrens, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of  
Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA

## FEATURES

source  
1..513  
/organism="Mus musculus"  
/mol\_type="mRNA"

/db\_xref="taxon:10090"  
/cell\_line="WEHI 265.1 RNA"

/note="alternatively spliced transcript of bcl-x long,  
GenBank Accession Number U10101"

gene  
1..513  
/genes="bcl-x long"

CDS  
1..513  
/genes="bcl-x long"

/codon\_start=1  
/product="bcl-x short"

/protein\_id="AA082172.1"

/db\_xref="GI:506646"

/translation="MQSNRELIVDFLSYKLSQKYSWSQFSQFSDVEENRTEAPEETEAE  
RETPSAINGNPWSHLADSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFLRYR  
RAPFSDTSQLHITPGTAYQSFQDTFVDLYGNNAAESRKQGRFNRFWLTGMTVAGV  
VLLGSLFSRK"

# ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 513;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||

Db 78 CTGACTCCAGCTGTATCC 61

## RESULT 7

LOCUS AF136230/c 513 bp mRNA linear ROD 01-JUN-1999  
DEFINITION Rattus norvegicus bcl-x short mRNA, complete cds.  
ACCESSION AF136230  
VERSION AF136230.1 GI:4928687

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 513)

AUTHORS He, X.J., Jin, K.L., Graham, S.H. and Simon, R.P.

TITLE Direct Submission  
JOURNAL Submitted (22-MAR-1999) Neurology, University of Pittsburgh, 3500  
Terrace Street, Pittsburgh, PA 15213, USA

## FEATURES

source  
1..513  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/tissue\_type="brain"  
/note="Isolated from an ischemic brain"

# CDS

1..513  
/codon\_start=1  
/product="bcl-x short"

/protein\_id="AAD33683.1"

/db\_xref="GI:4928688"

/translation="MQSNRELIVDFLSYKLSQKYSWSQFSQFSDVEENRTEAPEETEPE  
RETPSAINGNPWSHLADSPAVNGATGHSSSLDAREVTPMAAVKQALREAGDEFLRYR  
RAPFSDTSQLHITPGTAYQSFQDTFVDLYGNNAAESRKQGRFNRFWLTGMTVAGV  
VLLGSLFSRK"

# ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 513;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
|||||

Db 78 CTGACTCCAGCTGTATCC 61

## RESULT 8



```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 22596 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
              = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
              HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 12
LOCUS      CQ185831 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION  CQ185831
VERSION     CQ185831.1 GI:41180846
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 17227 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
              1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
              BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 13
LOCUS      CQ235904 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION  CQ235904
VERSION     CQ235904.1 GI:41219182
KEYWORDS
SOURCE      Homo sapiens (human)

```

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
              Patent: WO 0157273-A 22743 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
              = 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
              HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 14
LOCUS      CQ273477 555 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21738 from Patent WO0157277.
ACCESSION  CQ273477
VERSION     CQ273477.1 GI:41246081
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Acemica, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..555
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
              HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 487 CTGACTCCAGCTGTATCC 504

```

RESULT 15  
CQ310858  
LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21963 from Patent WO0186003.  
ACCESSION CQ310858  
VERSION CQ310858.1 GI:41271435  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Penn.S.G., Hanzel.D.K., Chen.W. and Rank.D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
TITLE analysis of gene expression in human lung  
JOURNAL Patent: WO 0186003-A 21963 15-NOV-2001;  
FEATURES  
source  
1. .555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =  
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 487 CTGACTCCAGCTGTATCC 504

Search completed: February 4, 2005, 23:30:41  
Job time : 432.664 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-8  
Perfect score: 18  
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAZ46978	Bcl-XL mr
2	18	100.0	65	ABN55935	Mouse spl
3	18	100.0	555	ABA73433	Human foe
4	18	100.0	555	Aai53868	Probe #22
5	18	100.0	555	ABA38761	Probe #17
6	18	100.0	555	AAK48039	Human bon
7	18	100.0	555	AAK21876	Human bra
8	18	100.0	555	ABS47753	Human liv
9	18	100.0	555	ABS21972	Human gen
10	18	100.0	559	ACH73889	Human gen
11	18	100.0	564	ACH87595	Human gen
12	18	100.0	600	ABA60917	Human foe
13	18	100.0	600	Aai40812	Probe #94
14	18	100.0	600	ABA28894	Probe #73
15	18	100.0	600	AAK35096	Human bon
16	18	100.0	600	AAK09207	Human bra
17	18	100.0	600	ABA34848	Human liv
18	18	100.0	600	ABS09558	Human gen
c 19	18	100.0	600	ADH52636	Chinese h
c 20	18	100.0	660	ADH52638	Chinese h
c 21	18	100.0	660	ADH52640	Chinese h

ALIGNMENTS

RESULT 1  
AAZ46978  
ID AAZ46978 standard; DNA; 18 BP.  
XX  
AC AAZ46978;  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-XL mRNA specific antisense oligo H.  
XX  
KW Anti-apoptotic protein; bcl-XL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
FI Stein CA;  
XX  
DR WPI; 2000-137140/12.  
XX  
PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-XL, useful for reducing bcl-XL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
XX  
PS Claim 1; Fig 1; 69pp; English.  
XX  
CC The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-XL. The oligonucleotides can be introduced into tumour cells to reduce bcl-XL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-XL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-XL production to promote the regression of vascular

Abt09346 Phase-1 R  
Aah43464 cDNA cion  
Adm45994 Human apo  
Aag81699 Human thy  
Abz83507 Toxicolog  
Adi32132 Human CDN  
Adg5218 Human Bcl  
Aaf30926 Human Bcl  
Adg5209 Human Bcl  
Adh52632 Chinese h  
Aag81698 Human thy  
Aat40079 Bcl-XL ge  
Aaz93614 Bcl-x gen  
Aas15189 Human Bcl  
Aac90810 Human Bcl  
Abk84766 Human CDN  
Abt16641 Human bcl  
Add56779 Human bcl  
Ad64187 Human bcl  
Adi32104 Human CDN  
Adh52630 Human ant  
Ado19990 Human PRO  
Adp13351 Renal cel  
Aas00247 Bcl-XL-DT

CC lesions. They can also be included with a carrier (and optionally tetra  
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
CC represent antisense oligos specific for the bcl-X1 mRNA

XX  
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 1 CTGACTCCAGCTGTATCC 18

## RESULT 2

ABN55935/c

ID ABN55935 standard; DNA; 65 BP.

XX

AC ABN55935;

XX

DT 15-JUL-2002 (first entry)

XX

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28683.

XX

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX

KW splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Mus musculus.

XX

PN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-IB001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

XX

PR 02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

DR WPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which

XX

PT selectively hybridize to mRNAs transcribed from a transcription unit of a

XX

PT genome, useful for detecting tissue-, pathology-, and developmental-

XX

PT specific genes.

XX

PS Example 1; SEQ ID NO 28683; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for detecting

XX

CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-

XX

CC )transcriptome comprises messenger RNAs transcribed from multiple

XX

CC transcription units that populate a genome. The library comprises several

XX

CC oligonucleotides, each capable of hybridizing selectively to a set of

XX

CC messenger RNAs transcribed from a given transcription unit of the genome,

XX

CC which encodes one or more messenger RNA splice variants. The

XX

CC oligonucleotide libraries are useful for detecting mRNAs from a

XX

CC biological sample, in expression profiling studies, in qualitatively or

XX

CC quantitatively characterizing the corresponding transcriptome, and in

XX

CC detecting RNA transcripts and splice variants of human or animal

XX

CC transcriptomes. The libraries may also be used as specialised mini

XX

CC libraries to detect transcripts of a sub-transcriptome under a particular

XX

CC biological or pathological state, and so allowing the detection of tissue

XX

CC - and pathology-specific genes such as those genes only expressed in

XX

CC specific tissue under a specific pathological condition; to detect

XX

CC developmental specific genes; and to detect RNA transcripts and splice

XX

CC variants of a transcriptome of a patient suffering from a particular

XX

CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from

XX

CC rats, humans and mice, which are used in the exemplification of the

XX

CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 65 BP; 19 A; 12 C; 20 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 65;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 31 CTGACTCCAGCTGTATCC 14

## RESULT 3

ABA73433

ID ABA73433 standard; DNA; 555 BP.

XX

AC ABA73433;

XX

DT 01-FEB-2002 (first entry)

XX

DE Human foetal liver single exon nucleic acid probe #21738.

XX

KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX

OS Homo sapiens.

XX

PN WO200157277-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000669.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-483447/52.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX

PT gene expression in human fetal liver.

XX

PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX

CC The invention relates to a single exon nucleic acid probe for measuring

XX

CC single exon nucleic acid probes may be used for predicting, measuring and

XX

CC displaying gene expression in samples derived from human fetal liver. The

XX

CC present sequence is a single exon nucleic acid probe of the invention.

XX

CC Note: The sequence data for this patent did not form part of the printed

XX

CC specification, but was obtained in electronic format directly from WIPO

XX

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
|||||  
Db 487 CTGACTCCAGCTGTATCC 504



AA  
XX  
PN

09-AUG-2001.

09-AUG-2001.  
PF  
PP  
FF  
XX

04-FEB-2000; 2000US-0180312P.  
PR  
26-MAY-2000; 2000US-0207456P.  
PR  
30-JUN-2000; 2000US-00608408.  
PR  
03-AUG-2000; 2000US-00632366.  
PR  
21-SEP-2000; 2000US-0234687P.  
PR  
27-SEP-2000; 2000US-0236359P.  
PR  
04-OCT-2000; 2000GB-00024263.  
PR  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
TT hearts.  
XX  
PS Claim 4; SEQ ID NO 17227; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
Best Local Similarity 100.0%; Pred.No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 CTGACTCCAGCTGTATCC 18  
|||  
DB 487 CTGACTCCAGCTGTATCC 504

RESULT 6  
AAK48039  
ID AAK48039 standard; DNA; 555 BP.  
AC  
XX AAK48039;  
XX AC  
DT DT  
DE DE  
XX Human bone marrow expressed single exon probe SEQ ID NO: 22596.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX Homo sapiens.  
OS  
XX WO200157276-A2.  
PN  
PD PD  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US0006568.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR

PS 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
CC 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488900/53.  
XX  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.  
PT  
PS Example 4; SEQ ID NO 22596; 659pp + Sequence Listing; English.  
XX  
XX The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in brain cell samples, CC samples, which may enable the improved diagnosis and treatment of cancers CC such as lymphoma, leukaemia and myeloma. The present sequence is one of CC the probes of the invention  
XX  
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 4; Length 555;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 7  
AAK21876  
ID AAK21876 standard; DNA; 555 BP.  
XX  
AC AAK21876;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe SEQ ID NO: 21867.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KW ss.  
XX Homo sapiens.  
OS  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-483446/52.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human brains.

PS Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, CC epilepsy and cancers. The present sequence is one of the probes of the CC invention  
XX  
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 4; Length 555;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 8  
ABS47753  
ID ABS47753 standard; DNA; 555 BP.  
XX  
AC ABS47753;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human liver single exon probe, SEQ ID No 22743.  
XX  
KW Human; single exon nucleic acid probe; liver; cirrhosis;  
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157273-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000664.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488998/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.  
PS  
PS Claim 4; SEQ ID NO 22743; 658pp; English.  
XX  
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for measuring human gene expression in a sample derived from human adult CC liver, comprising one of 13109 defined nucleotide sequences given in the CC specification (or complements/ fragments). The probe hybridises at high CC stringency to a nucleic acid molecule expressed in the human adult liver. CC (I) may be used for predicting, measuring and displaying gene expression CC in samples derived from human adult liver. The genes identified may be CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is CC associated with coronary heart disease. ABS25011-ABS51005 represent human CC liver single exon nucleic acid probes of the invention. Note: The CC

CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
 |||||  
 Db 487 CTGACTCCAGCTGTATCC 504

RESULT 9  
 ABS21972  
 ID ABS21972 standard; DNA; 555 BP.  
 AC ABS21972;  
 DT 19-AUG-2002 (first entry)  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.  
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease; open reading frame; ORF.

XX OS Homo sapiens.  
 XX WO200186003-A2.  
 PN 15-NOV-2001.  
 PD 30-JAN-2001; 2001WO-US000665.  
 PF 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-0060840B.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2002-114183/15.  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX Claim 4; SEQ ID NO 21963; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18  
 |||||  
 Db 487 CTGACTCCAGCTGTATCC 504

RESULT 10  
 ACH73889  
 ID ACH73889 standard; DNA; 559 BP.  
 AC ACH73889;  
 XX 29-JUL-2004 (first entry)  
 DT Human genome derived single exon probe #7084.  
 DE Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX Homo sapiens.  
 OS US2003194704-A1.  
 PN 16-OCT-2003.  
 PD 03-APR-2002; 2002US-00029386.  
 PF 03-APR-2002; 2002US-00029386.  
 PR (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX Penn SG, Rank DR, Hanzel DK;  
 DR WPI; 2004-119264/12.  
 XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for

```

PT surveying tissues.
XX
XX Claim 15; SEQ ID NO 7084; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX SQ Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 12; Length 559;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
| | | | | | | | | | | | | | | |
Db 82 CTGACTCCAGCTGTATCC 99

RESULT 11
ID ACH87595 standard; DNA; 564 BP.
XX
XX ACH87595;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #20790.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX

```

```

XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterising
XX alternative splicing events, in detecting and characterising gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX SQ Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18
| | | | | | | | | | | | | | | |
Db 487 CTGACTCCAGCTGTATCC 504

RESULT 12
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #9222.
XX

```

KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX Homo sapiens.  
 OS WO200157277-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000669.  
 PF 04-FEB-2000; 2000US-0180312P.  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human fetal liver.  
 XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.  
 XX The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 4; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTGACTCCAGCTGTATCC 18  
 Db 506 CTGACTCCAGCTGTATCC 523  
 RESULT 13  
 AAI40812  
 ID AAI40812 standard; DNA; 600 BP.  
 XX  
 AC AAI40812;  
 XX 17-OCT-2001 (first entry)  
 DT Probe #9498 used to measure gene expression in human placenta sample.  
 XX Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 XX Homo sapiens.  
 OS WO200157272-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000663.  
 PF 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488899/53.  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human placenta.  
 XX Claim 1; SEQ ID NO 9498; 654pp; English.  
 XX The present invention relates to single exon nucleic acid probes (SENPs).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders  
 XX  
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 4; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTGACTCCAGCTGTATCC 18  
 Db 506 CTGACTCCAGCTGTATCC 523  
 RESULT 14  
 ABA28894  
 ID ABA28894 standard; DNA; 600 BP.  
 XX  
 AC ABA28894;  
 XX 23-JAN-2002 (first entry)  
 DT Probe #7360 for gene expression analysis in human heart cell sample.  
 XX Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.  
 XX Homo sapiens.  
 OS WO200157274-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000666.  
 PF 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488899/53.  
 DR Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts.  
 XX Claim 1; SEQ ID NO 7360; 530pp; English.

PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human placenta.  
 XX Claim 25; SEQ ID NO 9498; 654pp; English.  
 XX The present invention relates to single exon nucleic acid probes (SENPs).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders  
 XX  
 SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 4; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTGACTCCAGCTGTATCC 18  
 Db 506 CTGACTCCAGCTGTATCC 523  
 RESULT 14  
 ABA28894  
 ID ABA28894 standard; DNA; 600 BP.  
 XX  
 AC ABA28894;  
 XX 23-JAN-2002 (first entry)  
 DT Probe #7360 for gene expression analysis in human heart cell sample.  
 XX Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.  
 XX Homo sapiens.  
 OS WO200157274-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000666.  
 PF 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488899/53.  
 DR Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts.  
 XX Claim 1; SEQ ID NO 7360; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
Db 506 CTGACTCCAGCTGTATCC 523

## RESULT 15

AAK35096  
ID AAK35096 standard; DNA; 600 BP.

XX AC AAK35096;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 9653.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
XX probes which are derived from genomic sequences expressed in the human  
XX bone marrow. They can be used to measure gene expression in bone marrow  
XX samples, which may enable the improved diagnosis and treatment of cancers  
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of  
XX the probes of the invention

XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18  
Db 506 CTGACTCCAGCTGTATCC 523

Search completed: February 4, 2005, 21:52:43  
Job time : 233.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-8  
Perfect score: 18  
Sequence: 1 ctgactccagctgtatcc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_ges1:\*
- 9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	279	2	AW247015 2822471.5
C 2	18	100.0	287	5	BY236510
C 3	18	100.0	313	6	CF171262
C 4	18	100.0	320	5	BY220922
C 5	18	100.0	322	2	AW125200
C 6	18	100.0	325	5	BY191347
C 7	18	100.0	327	5	BY209882
C 8	18	100.0	336	5	BY219527
C 9	18	100.0	339	1	AA232598
C 10	18	100.0	341	5	BY176914
C 11	18	100.0	344	2	BB869154
C 12	18	100.0	348	5	BY010071
C 13	18	100.0	350	5	BY058101
C 14	18	100.0	353	5	BY016163
C 15	18	100.0	355	5	BY180189
C 16	18	100.0	355	5	BY212491
C 17	18	100.0	356	5	BY180646
C 18	18	100.0	357	2	BB870590
C 19	18	100.0	358	5	BY203613
C 20	18	100.0	361	5	BY176753
C 21	18	100.0	363	5	BY221240
C 22	18	100.0	363	5	BY293078
C 23	18	100.0	367	2	BB843018
C 24	18	100.0	368	5	BY178528

C 25	18	100.0	369	5	BY174511
C 26	18	100.0	374	2	BB844512
C 27	18	100.0	374	5	BY055234
C 28	18	100.0	378	2	BB871778
C 29	18	100.0	382	2	BB842471
C 30	18	100.0	382	4	BM855440
C 31	18	100.0	391	2	BE253353
C 32	18	100.0	391	5	BY096186
C 33	18	100.0	391	6	CB775315
C 34	18	100.0	394	6	CD540521
C 35	18	100.0	395	4	BI030877
C 36	18	100.0	402	6	CB769704
C 37	18	100.0	407	7	CN422267
C 38	18	100.0	408	5	BY298104
C 39	18	100.0	408	6	CA558426
C 40	18	100.0	414	2	BF523847
C 41	18	100.0	421	4	BM844286
C 42	18	100.0	421	6	CF145335
C 43	18	100.0	422	5	BY281787
C 44	18	100.0	425	5	BY287181
C 45	18	100.0	431	6	CA896103

## ALIGNMENTS

RESULT 1  
LOCUS AW247015/c  
DEFINITION 2822471.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822471 5', mRNA sequence.  
ACCESSION AW247015  
VERSION AW247015.1 GI:6590008  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 279)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2822471.3prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project. Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu  
Plate: LLCM9 row: H column: 24  
High quality sequence stop: 199.  
Location/Qualifiers  
1. 279  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822471"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18

|||||  
134 CTGACTCCAGCTGTATCC 117

## RESULT 2

BY236510/c

LOCUS

DEFINITION BY236510 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930048G15 5', mRNA sequence.

ACCESSION BY236510

VERSION BY236510.1

KEYWORDS GI:26417686

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 287)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,

Saitana, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shingawa, J., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

PUBLISHED

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

## FEATURES

source

1. .287

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="F930048G15"

/tissue\_type="inner ear"

/dev\_stage="adult"

/clone\_lib="RIKEN full-length enriched, adult inner ear"

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 287;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18

|||||

138 CTGACTCCAGCTGTATCC 121

Db

RESULT 3

CF171262/c

LOCUS

DEFINITION

musculus cDNA clone NIA:B0840B09 IMAGE:30471284 5', mRNA sequence.

CF171262

VERSION

CF171262.1

GI:33280811

EST.

Mus musculus (house mouse)

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 313)

Piao, Y., KO, N. T., Lim, M. K. and KO, M. S. H.

Subconstruction of long-transcript enriched cDNA libraries from

submicrogram amounts of total RNAs by a universal PCR amplification

method

Genome Res. 11 (9), 1553-1558 (2001)

21429098

PUBLISHED

COMMENT

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgaun.grc.nia.nih.gov

Plate: B0840 row: B column: 09

Seq primer: M13 Reverse

High quality sequence stop: 313

POLYA=No.

Location/Qualifiers

1. .313

/organism="Mus musculus"



/mol\_type="mRNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="NIA:B0840B09 IMAGE:30471284"  
/dev\_stage="Newborn Kidney"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Newborn Kidney cDNA Library (Long 1)"  
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). In brief, double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]:  
5'-pGACTAGTCTAGTCGAGCGCGCCCTTTT-3' from 26 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 313;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 45 CTGACTCCAGCTGTATCC 28

## RESULT 4

BY220922/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY220922 320 bp mRNA linear EST 10-DEC-2002  
BY220922 RIKEN full-length enriched, activated spleen Mus musculus  
cDNA clone F830217H02 5', mRNA sequence.

BY220922

BY220922.1 GI:26402025

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 320)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sulcane, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683

## PUBMED

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

## FEATURES

## source

Location/Qualifiers  
1..320  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="NOD"  
/db\_xref="taxon:10090"  
/clone="F830217H02"  
/tissue type="activated spleen"  
/clone\_lib="RIKEN full-length enriched, activated spleen"

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 320;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 276 CTGACTCCAGCTGTATCC 259

## RESULT 5

AW125200/c

LOCUS

DEFINITION

AW125200 322 bp mRNA linear EST 22-OCT-1999

UI-M-BH2.1-aps-a-07-0-UI.61 NIH BMAP M.S3.1 Mus musculus cDNA clone

UI-M-BH2.1-aps-a-07-0-UI.3', mRNA sequence.

Accession	AW125200	Best Local Similarity	100.0%;	Pred. No.	1.8e+02;	Mismatches	0;	Indels	0;	Gaps	0;
Version	AW125200.1	GI:6100730									
Keywords	EST.										
Source	Mus musculus										
Organism	Mus musculus (house mouse)										
Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 322)										
Authors	Bonaldo,M.F., Lennon,G. and Soares,M.B.										
Title	Normalization and subtraction: two approaches to facilitate gene discovery										
Journal	Genome Res. 6 (9), 791-806 (1996)										
Medline	97044477										
PubMed	8889548										
Comment	Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: mEST@mail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA=Yes.										
Features	Location/Qualifiers										
Source	1..322										
	/organism="Mus musculus"										
	/mol_type="mRNA"										
	/strain="C57BL/6J"										
	/db_xref="taxon:10090"										
	/clone="UI-M-BH2.1-aps-a-07-0-UI"										
	/dev_stage="27-32 days"										
	/lab_host="DH10B (Life Technologies)"										
	/clone_lib="NIH BMAP M S3.1"										
	/note="Vector: pTT30-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI: The NIH_BMAP_M_S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)										
	TAG_TISSUE=brain-stems										
	TAG_LIB=NIH_BMAP_M_S3.1										
	TAG_SEQ=TCGA"										
Origin	Query Match										
	100.0%;	Score	18;	DB	2;	Length	322;				

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

## source

1. 325  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="NOD"  
 /db\_xref="taxon:10090"  
 /clone="F630320F03"  
 /cell\_type="NOD-derived CD11c +ve dendritic cells"  
 /clone\_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 263 CTGACTCCAGCTGTATCC 246

## RESULT 7

## LOCUS

BY209882/c  
 BY209882 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730312F08 5', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 327)  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oeato, N., Saito, R., Suzuki, H., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V., Chohta, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guatinchich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nunata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pilla, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reid, J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: [genome-res@gsc.riken.jp](mailto:genome-res@gsc.riken.jp), URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

## source

1. 327  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="F730312F08"  
 /cell\_type="B6-derived CD11 +ve dendritic cells"  
 /clone\_lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTCCAGCTGTATCC 18

Db 288 CTGACTCCAGCTGTATCC 271

## RESULT 8

## LOCUS

## DEFINITION

## ACCESSION

BY219527/c  
 BY219527 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830115M14 5', mRNA sequence.

BY219527 336 bp mRNA linear EST 10-DEC-2002

VERSION BY219527.1 GI:26400547  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojibori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Ciothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Negashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Resole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varado, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, B.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 NATURE 420, 563-573 (2002)

JOURNAL 22354683  
 MEDLINE 12466851  
 PUBMED

COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)  
 Normalize and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

FEATURES  
 Source  
 1. .339  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5426748"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:664718"  
 /tissue\_type="neuroepithelial cells"  
 /dev\_stage="Ntera-2 neuroepithelial cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene NT2 neuronal precursor 937230"  
 /note="Organ: brain; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;

ORIGIN  
 Query Match 100.0%; Score 18; DB 5; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0;

QY 1 CTGACTCCAGCTGTATCC 18  
 |||||  
 Db 278 CTGACTCCAGCTGTATCC 261

RESULT 9  
 AA232598/c  
 LOCUS  
 DEFINITION  
 zxr28c08.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens  
 CDNA clone IMAGE:664718 5' similar to TR:G998484 G998484  
 BCL-XSHTO-APOPTOSIS INDUCER ; mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

AA232598 339 bp mRNA linear EST 28-FEB-1997  
 zxr28c08.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens  
 CDNA clone IMAGE:664718 5' similar to TR:G998484 G998484  
 BCL-XSHTO-APOPTOSIS INDUCER ; mRNA sequence.  
 AA232598  
 AA232598.1 GI:1855453  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 339)  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevas, K., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 8889549  
 97044478  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28ml3 rev1 ET from Amersham  
 High quality sequence stop: 175.  
 Location/Qualifiers  
 1. .339  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5426748"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:664718"  
 /tissue\_type="neuroepithelial cells"  
 /dev\_stage="Ntera-2 neuroepithelial cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene NT2 neuronal precursor 937230"  
 /note="Organ: brain; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG  
3' -3' adaptor sequence: 5' CTCAGTGTGTGTGTGTGTGTGT 3'

## ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 339;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCAGCTGTATCC 18

|||||

Db 300 CTGACTCAGCTGTATCC 283

## RESULT 10

BY176914/c

LOCUS

DEFINITION BY176914 RIKEN full-length enriched, NOD-derived CD11c +ve  
dendritic cells Mus musculus cDNA clone F630021E08 5', mRNA  
sequence.

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Okazaki, Y., Furuno, M., Sasakawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusci, V.,  
Chocho, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Vezardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC Building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

## FEATURES

source

Location/Qualifiers  
1..341  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="NOD"  
/db\_xref="taxon:10090"  
/clone="F630021E08"  
/cell\_type="NOD-derived CD11c +ve dendritic cells"  
/clone\_lib="RIKEN full-length enriched, NOD-derived CD11c  
+ve dendritic cells"

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 341;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCAGCTGTATCC 18

|||||

Db 294 CTGACTCAGCTGTATCC 277

## RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

<p>Tel: 81-45-503-9222  Fax: 81-45-503-9216  Email: genome-res@gscc.riken.jp, URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a>  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsura, S., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  Please visit our web site (<a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a>) for further details.  e mouse tissues.</p>		<p>REFERENCE  AUTHORS</p>		<p>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  1 (bases 1 to 348)  Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaudo, I., Ootani, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustigich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Negashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempel, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yaenishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  Nature 420, 563-573 (2002)  22354683  12466851</p>		<p>TITLE  JOURNAL  MEDLINE  PUBMED  COMMENT</p>		<p>CONTACT: Yoshihide Hayashizaki  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  The Institute of Physical and Chemical Research (RIKEN)  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  Tel: 81-45-503-9222  Fax: 81-45-503-9216  Email: genome-res@gscc.riken.jp, URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a>  Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  Please visit our web site (<a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a>) for further details.  Location/Qualifiers  1. .348  /organism="Mus musculus"  /mol_type="mRNA"  /db_xref="taxon:10090"  /clone="G730016N07"  /tissue_type="lung"</p>		<p>FEATURES  source</p>		<p>Query Match 100.0%; Score 18; DB 2; Length 344;  Best Local Similarity 100.0%; Pred. No. 1.8e+02;  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		<p>Qy 1 CTGACTCCAGCTGTATCC 18         Db 219 CTGACTCCAGCTGTATCC 202       </p>		<p>RESULT 12  BY010071/c  LOCUS  DEFINITION BY010071 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus  musculus cDNA clone G730016N07 5', mRNA sequence.  ACCESSION BY010071.1 GI:26070320  VERSION BY010071.1  KEYWORDS Mus musculus (house mouse)  SOURCE Mus musculus  ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p>	
---	--	-------------------------------	--	---	--	---	--	---	--	-----------------------------	--	---	--	--	--	--	--



```

/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
cDNA"

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 288 CTGACTCCAGCTGTATCC 271

RESULT 13
BY058101/c
LOCUS
DEFINITION
350 bp mRNA linear EST 06-DEC-2002
clone I730095E04 5', mRNA sequence.

ACCESSION
BY058101
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Baldarelli, R., Hill, D.P., Bult, C.,
Schonbach, C., Gojobori, T., Schriml, L.M., Kanapin, A., Matsuda, H.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Santana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physiological and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission

```

```

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source
1. 350
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="I730095E04"
/cell_line="TIB-55 BB88"
/clone_lib="RIKEN full-length enriched, TIB-55 BB88"

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACTCCAGCTGTATCC 18
|||||
Db 280 CTGACTCCAGCTGTATCC 263

RESULT 14
BY016163/c
LOCUS
DEFINITION
353 bp mRNA linear EST 06-DEC-2002
BY016163 RIKEN full-length enriched, mammary gland RCB-0526
Jyg-MC(A) cDNA Mus musculus cDNA clone G830015P06 5', mRNA
sequence.

ACCESSION
BY016163
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 353)

REFERENCE
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Baldarelli, R., Hill, D.P., Bult, C.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Santana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physiological and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission

```





```
FEATURES
source
Location/Qualifiers
1. .355
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630038P12"
/cell_type="NOD-derived.CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"

ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 355;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACTCCAGCTGTATCC 18
   |||||
Db 263 CTGACTCCAGCTGTATCC 246

Search completed: February 5, 2005, 08:11:48
Job time : 2149.2 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-9  
Perfect score: 18  
Sequence: 1 ggtctccatctccgattc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235157
2	18	100.0	18	6	BD235175
3	18	100.0	18	6	BD235176
c 4	18	100.0	512	6	CO727769 Sequence
5	18	100.0	555	6	CQ113695
6	18	100.0	555	6	CQ152574
7	18	100.0	555	6	CQ185831
8	18	100.0	555	6	CQ235904
9	18	100.0	555	6	CQ273477
10	18	100.0	555	6	CQ310858
11	18	100.0	555	6	CQ347773
12	18	100.0	600	6	CQ100639
13	18	100.0	600	6	CQ139631
14	18	100.0	600	6	CQ175964
15	18	100.0	600	6	CQ222999
16	18	100.0	600	6	CQ260961
17	18	100.0	600	6	CQ298444
18	18	100.0	600	6	CQ335104
c 19	18	100.0	636	6	BD097037

c 20	18	100.0	702	6	BD084108	BD084108 Method of
c 21	18	100.0	702	6	BD102202	BD102202 Method fo
c 22	18	100.0	702	9	BT007208	BT007208 Homo sapi
c 23	18	100.0	702	12	BT008248	BT008248 Synthetic
c 24	18	100.0	723	9	HSU72398	U72398 Human Rcl-x
c 25	18	100.0	737	6	AR054022	AR054022 Sequence
c 26	18	100.0	737	6	AR172595	AR172595 Sequence
c 27	18	100.0	737	6	IS2012	IS2012 Sequence 7
c 28	18	100.0	737	6	AR371662	AR371662 Sequence
c 29	18	100.0	737	6	AR380913	AR380913 Sequence
c 30	18	100.0	737	9	HSBCLXS	Z31116 H. sapiens b
c 31	18	100.0	747	6	AX127722	AX127722 Sequence
c 32	18	100.0	926	6	AR054021	AR054021 Sequence
c 33	18	100.0	926	6	AR118504	AR118504 Sequence
c 34	18	100.0	926	6	AR124952	AR124952 Sequence
c 35	18	100.0	926	6	AR144311	AR144311 Sequence
c 36	18	100.0	926	6	AR172594	AR172594 Sequence
c 37	18	100.0	926	6	BD243042	BD243042 Antisense
c 38	18	100.0	926	6	CQ765842	CQ765842 Sequence
c 39	18	100.0	926	6	E58777	E58777 Screening m
c 40	18	100.0	926	6	IS2011	IS2011 Sequence 5
c 41	18	100.0	926	6	AR380885	AR380885 Sequence
c 42	18	100.0	926	6	AX839772	AX839772 Sequence
c 43	18	100.0	926	6	AX925686	AX925686 Sequence
c 44	18	100.0	926	9	HSBCLXL	Z23115 H. sapiens b
c 45	18	100.0	1236	6	AX085490	AX085490 Sequence

#### ALIGNMENTS

RESULT 1  
BD235157  
LOCUS BD235157 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235157  
VERSION BD235157.1 GI:33044927  
KEYWORDS JP 2002519048-A/9.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 9 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/9  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC

C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC  
A61K47/42,  
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence',  
Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

#### FEATURES

#### ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGTCTCCATCTCCGATTTC 18  
|||||||

```

Db      1  GGTCTCCATCTCCGATTC 18

RESULT 2
BD235175
LOCUS      18 bp      DNA
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235175
VERSION     BD235175.1 GI:33044945
KEYWORDS   JP 2002519048-A/27.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein, C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 27 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/27
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
           C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
           A61K47/42,
           PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
           CC ANTISENSE OLIGONUCLEOTIDE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           CC PHOSPHOROTHIOATE LINKAGE
           FH Key Location/Qualifiers
           FT misc_binding (1)..(4)
           FT misc_binding (5)..(7)
           FT misc_binding (9)..(10)
           FT misc_binding (11)..(12)
           FT misc_binding (15)..(18)
           FT modified_base (3)..(3)
           FT modified_base (4)..(4)
           FT modified_base (6)..(7)
           FT modified_base (5)..(5)
           FT modified_base (9)..(9)
           FT modified_base (10)..(10)
           FT modified_base (11)..(11)
           FT modified_base (12)..(13)
           FT modified_base (16)..(17).
FEATURES
  source
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
  Query Match 100.0%; Score 18; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 59;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCTCCATCTCCGATTC 18
      |||
      1  GGTCTCCATCTCCGATTC 18

RESULT 4
BD235176
LOCUS      512 bp      DNA
DEFINITION Sequence 13703 from Patent WO02068579.
ACCESSION  CQ727769
VERSION     CQ727769.1 GI:42294740
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Venter C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
           humanexons or transcripts, for detecting expression and other uses
           thereof
JOURNAL    Patent: WO 02068579-A 13703 06-SEP-2002;
           PE Corporation (NV) (US)
FEATURES
  Location/Qualifiers
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
  Query Match 100.0%; Score 18; DB 6; Length 18;
  Best Local Similarity 100.0%; Pred. No. 59;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCTCCATCTCCGATTC 18
      |||
      1  GGTCTCCATCTCCGATTC 18

```

```

source
1. 512
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 512;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 275 GGTCTCCATCTCCGATTC 258

RESULT 5
CQ113695
LOCUS CQ113695 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 22554 from Patent WO0157272.
ACCESSION CQ113695
VERSION CQ113695.1 GI:41083565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 22554 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1. 555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 6
CQ152574
LOCUS CQ152574 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 22596 from Patent WO0157276.
ACCESSION CQ152574
VERSION CQ152574.1 GI:41159924
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 22596 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1. 555
/organism="Homo sapiens"
/mol_type="unassigned DNA"

source
1. 555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 7
CQ185831
LOCUS CQ185831 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17227 from Patent WO0157274.
ACCESSION CQ185831
VERSION CQ185831.1 GI:41180846
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 17227 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1. 555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =
1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
|||||
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 8
CQ235904
LOCUS CQ235904 555 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 22743 from Patent WO0157273.
ACCESSION CQ235904
VERSION CQ235904.1 GI:41219182
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000

```

(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
Patent: WO 0157273-A 22743 09-AUG-2001;  
Aeomica, Inc. (US)

FEATURES  
source  
Location/Qualifiers  
1. .555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL  
= 1.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN  
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
|||||  
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 9  
LOCUS CQ273477 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21738 from Patent WO0157277.  
ACCESSION CQ273477  
VERSION CQ273477.1 GI:41246081  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human fetal liver  
JOURNAL Patent: WO 0157277-A 21738 09-AUG-2001;  
Aeomica, Inc. (US)

FEATURES  
source  
Location/Qualifiers  
1. .555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL  
= 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN  
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
|||||  
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 10  
LOCUS CQ310858 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21963 from Patent WO0186003.  
ACCESSION CQ310858  
VERSION CQ310858.1 GI:41271435  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human lung  
Patent: WO 0186003-A 21963 15-NOV-2001;  
Aeomica, Inc. (US)

FEATURES  
source  
Location/Qualifiers  
1. .555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =  
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
|||||  
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 11  
LOCUS CQ347773 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21867 from Patent WO0157275.  
ACCESSION CQ347773  
VERSION CQ347773.1 GI:41296844  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 21867 09-AUG-2001;  
Aeomica, Inc. (US)

FEATURES  
source  
Location/Qualifiers  
1. .555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =  
1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:  
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE  
0.00e+00"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
|||||  
Db 424 GGTCTCCATCTCCGATTC 441

RESULT 12  
LOCUS CQ100639 600 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 9498 from Patent WO0157272.  
ACCESSION CQ100639  
VERSION CQ100639.1 GI:41069665  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
JOURNAL      Patent: WO 0157272-A 9498 09-AUG-2001;
              Aecomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..600
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
                0.99"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCTCCATCTCCGATTC 18
        |||||
Db      443 GGTCTCCATCTCCGATTC 460

RESULT 13
LOCUS      CQ139631                600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9653 from Patent WO0157276.
ACCESSION  CQ139631
VERSION     CQ139631.1 GI:41097003
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human bone marrow
JOURNAL      Patent: WO 0157276-A 9653 09-AUG-2001;
              Aecomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..600
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
                = 4.7"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCTCCATCTCCGATTC 18
        |||||
Db      443 GGTCTCCATCTCCGATTC 460

RESULT 14
LOCUS      CQ175964                600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 7360 from Patent WO0157274.
ACCESSION  CQ175964
VERSION     CQ175964.1 GI:41170703
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
```

```
analysis of gene expression in human heart
JOURNAL      Patent: WO 0157274-A 7360 09-AUG-2001;
              Aecomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..600
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCTCCATCTCCGATTC 18
        |||||
Db      443 GGTCTCCATCTCCGATTC 460

RESULT 15
LOCUS      CQ222999                600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9838 from Patent WO0157273.
ACCESSION  CQ222999
VERSION     CQ222999.1 GI:41205280
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
              ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
              3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
              60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
              August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
              (03.10.00)<150> US 60/236,359<151> 27 September 2000
              (27.09.00)<150> US 60/234,687<151> 21 September 2000
              (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
              Molecular Dynamics Sequence Listing Engine
JOURNAL      Patent: WO 0157273-A 9838 09-AUG-2001;
              Aecomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..600
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
                = 1.7"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCTCCATCTCCGATTC 18
        |||||
Db      443 GGTCTCCATCTCCGATTC 460

Search completed: February 4, 2005, 23:30:41
Job time : 432.664 secs
```

ORIGINAL LEFT BLANK



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-9  
Perfect score: 18  
Sequence: 1 ggctccatctccgattc 18  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	AZ46979 Bcl-Xl mR
2	18	100.0	555	4	ABA73433 Human foe
3	18	100.0	555	4	Aa153868 Probe #22
4	18	100.0	555	4	ABA38761 Probe #17
5	18	100.0	555	4	Aak48039 Human bon
6	18	100.0	555	4	Aak21876 Human bra
7	18	100.0	555	4	ABS47753 Human liv
8	18	100.0	555	6	ABS21972 Human gen
9	18	100.0	559	12	ACH73889 Human gen
10	18	100.0	564	12	ACH87595 Human gen
11	18	100.0	600	4	ABA60917 Human foe
12	18	100.0	600	4	Aa140812 Probe #94
13	18	100.0	600	4	ABA28894 Probe #73
14	18	100.0	600	4	Aak35096 Human bon
15	18	100.0	600	4	Aak09207 Human bra
16	18	100.0	600	4	ABe34848 Human liv
17	18	100.0	600	6	ABs09558 Human gen
18	18	100.0	636	4	Aah48169 Mutant bc
19	18	100.0	702	5	AH43464 cDNA clon
20	18	100.0	702	12	ADM45994 Human apo
21	18	100.0	737	2	AAQ81699 Human thy

C 22	18	100.0	737	10	ABZ83507
C 23	18	100.0	737	11	ADI32132
C 24	18	100.0	739	12	ADG65218
C 25	18	100.0	747	4	AAF30926
C 26	18	100.0	747	12	ADG65209
C 27	18	100.0	926	2	AAQ81698
C 28	18	100.0	926	2	AA740079
C 29	18	100.0	926	3	AAZ93614
C 30	18	100.0	926	4	AA515189
C 31	18	100.0	926	4	AAC90810
C 32	18	100.0	926	6	ABK84766
C 33	18	100.0	926	8	ABT16641
C 34	18	100.0	926	10	ADDS6779
C 35	18	100.0	926	10	AAE4187
C 36	18	100.0	926	11	ADI32104
C 37	18	100.0	926	12	ADH52630
C 38	18	100.0	926	12	ADO19990
C 39	18	100.0	926	12	ADP13351
C 40	18	100.0	1236	5	AA000247
C 41	18	100.0	1455	5	AA000250
C 42	18	100.0	2386	10	ADG89403
C 43	18	100.0	2386	12	ADN04260
C 44	18	100.0	2575	12	ADO19866
C 45	18	100.0	7372	2	AA333182

ALIGNMENTS

RESULT 1  
AAZ46979  
ID AAZ46979 standard; DNA; 18 BP.  
AC  
XX  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-Xl mRNA specific antisense oligo I.  
XX  
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
XX lung; bladder; bcl-2; vascular lesion; antisense; ss.  
OS Homo sapiens.  
XX  
XX  
PN WO200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Stein CA;  
XX  
XX WPI; 2000-137140/12.  
XX  
PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-  
XX xL, useful for reducing bcl-xL production in tumor cells to treat cancer  
XX or in vascular cells to promote the regression of vascular lesions.  
XX  
XX Claim 1; Fig 1; 69pp; English.  
XX  
XX The invention provides antisense oligonucleotides or their derivatives  
XX which reduce or eliminate expression of the anti-apoptotic protein bcl-  
XX xL. The oligonucleotides can be introduced into tumour cells to reduce  
XX bcl-xL production to treat cancer, especially epithelial cancer, e.g.  
XX prostate, lung or bladder cancer. Oligonucleotides comprising one or more  
XX bases with a C-5 propynyl pyrimidine modification may especially be used  
XX to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in  
XX such treatment. The oligonucleotides can be introduced into vascular  
XX cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX  
 SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18  
 |||||  
 Db 1 GGCTCCATCTCCGATTC 18

RESULT 2  
 ABA73433  
 ID ABA73433 standard; DNA; 555 BP.

XX  
 AC ABA73433;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #21738.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human foetal liver.

XX Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human foetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18  
 |||||  
 Db 424 GGCTCCATCTCCGATTC 441

RESULT 3  
 AA153868  
 ID AA153868 standard; DNA; 555 BP.

XX AA153868;

XX 17-OCT-2001 (first entry)

XX Probe #22554 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 22554; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCATCTCCGATTC 18  
 |||||  
 Db 424 GGCTCCATCTCCGATTC 441

RESULT 4  
 ABA38761  
 ID ABA38761 standard; DNA; 555 BP.

XX ABA38761;

XX 23-JAN-2002 (first entry)

XX Probe #17227 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
FA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
FT gene expression in human bone marrow.
PT
XX Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX Seq Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 1 GGTCCTCATCTCCGATTC 18
Db |||||
424 GGTCCTCATCTCCGATTC 441
RESULT 6
AAK21876
ID AAK21876 standard; DNA; 555 BP.
XX
AC AAK21876;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 21867.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
WO200157275-A2.
PN
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
FA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

```

```
XX Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
PS
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCCATCTCCGATTC 18
DB 424 GGCTCCCATCTCCGATTC 441
RESULT 7
ID ABS47753 standard; DNA; 555 BP.
XX ABS47753;
XX
DT 25-FEB-2003 (first entry)
DE Human liver single exon probe, SEQ ID NO 22743.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; HS.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-48898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 4; SEQ ID NO 22743; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (i) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
```

---

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCCATCTCCGATTC 18
DB 424 GGCTCCCATCTCCGATTC 441
RESULT 8
ID ABS21972 standard; DNA; 555 BP.
XX ABS21972;
XX
DT 19-AUG-2002 (first entry)
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21963.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagazer syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 21963; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
```

mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18  
|||||  
Db 424 GGCTCCATCTCCGATTC 441

# RESULT 9

ACH73889  
ID ACH73889 standard; DNA; 559 BP.

XX ACH73889;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #7084..

XX Human; probe; ss; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human  
XX gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for  
XX surveying tissues.

XX Claim 15; SEQ ID NO 7084; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene  
XX expression, comprising any of the 27,400 fully defined nucleotide  
XX sequences in the specification, or their complements or fragments, and  
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences  
XX fully defined in the specification. The probe is a single exon probe that  
XX hybridises under high stringency conditions to a nucleic acid molecule  
XX expressed in human cells or tissues. Also included are a spatially-  
XX addressable set of single exon nucleic acid probes for measuring human  
XX gene expression (comprising a plurality of single exon nucleic acid  
XX probes cited above, where each of the plurality of probes is separately  
XX and addressably isolatable or amplifiable from the plurality), a single  
XX exon microarray for measuring human gene expression, a method of  
XX measuring human gene expression, a vector comprising the single exon  
XX probe cited above, an ORF-encoded peptide comprising at least 8  
XX contiguous amino acids of any of the above-mentioned amino acid  
XX sequences (optionally with conservative amino acid substitutions), an  
XX isolated antibody that binds specifically to a peptide cited above,  
XX methods of selling and/or licensing single exon probes or microarrays to  
XX a customer desiring to measure gene expression, a method of providing  
XX human gene expression data by subscription, and a computer-readable  
XX storage medium which contains a database having a plurality of records  
XX (each record including data on the expression of a single exon probe  
XX cited above). The probe, methods and apparatus are useful in gene  
XX expression analysis. The probes may be used as tools for surveying  
XX tissues to detect the presence of expressed messages that contain their  
XX specific exon, or in constructing genome-derived single exon microarrays.  
XX In addition, the probes are used in identifying and characterising  
XX alternative splicing events, in detecting and characterising gross  
XX alterations in the genomic locus that includes their exon, in assessing  
XX smaller genomic alterations, in priming the synthesis of nucleic acids,  
XX or in expressing the ORF-encoded peptide. The present sequence is a human  
XX single exon probe of the invention. Note: The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from USPTO at  
XX seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 559;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCATCTCCGATTC 18

Db 19 GGCTCCATCTCCGATTC 36

# RESULT 10

ACH87595

ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

XX Human; probe; ss; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

```

PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 1; SEQ ID NO 20790; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 564;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCATCTCCGATTC 18
DB 424 GGCTCCATCTCCGATTC 441
RESULT 11
ABA60917
ID ABA60917 standard; DNA; 600 BP.
XX
XX ABA60917;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #9222.
DE

```

---

```

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX
XX Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCCATCTCCGATTC 18
DB 443 GGCTCCATCTCCGATTC 460
RESULT 12
AAI40812
ID AAI40812 standard; DNA; 600 BP.
XX
XX AAI40812;
XX
XX 17-OCT-2001 (first entry)
XX
XX Probe #9498 used to measure gene expression in human placenta sample.
DE
XX Probe: microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX

```

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632386.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 9498; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
Db 443 GGTCTCCATCTCCGATTC 460

RESULT 13
ID ABA28894
AC ABA28894;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #7360 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX

PS Claim 1; SEQ ID NO 7360; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCTCCATCTCCGATTC 18
Db 443 GGTCTCCATCTCCGATTC 460

RESULT 14
ID AAK35096
AC AAK35096;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18  
|||||  
Db 443 GGTCCTCATCTCCGATTC 460

## RESULT 15

AAK09207  
ID AAK09207 standard; DNA; 600 BP.  
XX  
AC AAK09207;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe SEQ ID NO: 9198.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.

XX  
PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.

XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention

XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18  
|||||  
Db 443 GGTCCTCATCTCCGATTC 460

Search completed: February 4, 2005, 21:52:43  
Job time : 232.23 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-9  
Perfect score: 18  
Sequence: 1 ggtctcatctccgattc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	243	4	BM409971 EST584298
2	18	100.0	279	2	AW247015 2822471.5
3	18	100.0	344	8	A2576742 AST-2T009
4	18	100.0	382	4	BM855440 K-EST0138
5	18	100.0	408	2	AW933481 EST359240
6	18	100.0	421	4	BM844286 K-EST0122
7	18	100.0	421	6	CF145335 UI-HF-CB0
8	18	100.0	453	2	AW930419 EST340792
9	18	100.0	455	1	AI777656 EST258451
10	18	100.0	474	7	CM422261 170004245
11	18	100.0	503	1	AI283063 qm62c06.x
12	18	100.0	503	4	BM857244 K-EST0141
13	18	100.0	542	7	CM422262 170004245
14	18	100.0	560	6	CD675630 fs25h07.Y
15	18	100.0	571	2	AW931273 EST351116
16	18	100.0	577	6	CF131978 UI-HF-FQ0
17	18	100.0	584	1	AI134785 DKEP347K
18	18	100.0	587	2	AW931455 EST357298
19	18	100.0	587	2	BE871836 601447837
20	18	100.0	596	2	AW442063 EST3111459
21	18	100.0	596	2	AW732926 bb17b09.Y
22	18	100.0	597	2	AW930783 EST356626
23	18	100.0	597	2	AW931219 EST357062
24	18	100.0	603	2	AW930433 EST340806

25	18	100.0	605	2	AW931446
c 26	18	100.0	606	7	CN422268
c 27	18	100.0	612	2	BE783664
c 28	18	100.0	614	2	BE206897
c 29	18	100.0	616	6	CF132307
c 30	18	100.0	624	6	CF131456
c 31	18	100.0	632	7	CN422264
c 32	18	100.0	635	4	BI489889
c 33	18	100.0	638	4	BI924992
c 34	18	100.0	657	2	BE207063
c 35	18	100.0	671	2	AW814739
c 36	18	100.0	688	4	BG708652
c 37	18	100.0	688	4	BM409531
c 38	18	100.0	697	4	BI457116
c 39	18	100.0	697	5	BU184922
c 40	18	100.0	700	4	BG831301
c 41	18	100.0	702	6	CF125275
c 42	18	100.0	704	4	BI561500
c 43	18	100.0	707	6	CD636467
c 44	18	100.0	711	2	BE535474
c 45	18	100.0	720	6	CD636470

## ALIGNMENTS

## RESULT 1

## BM409971

## LOCUS

## DEFINITION

## ACCSSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Seq primer: T3.

## Location/Qualifiers

## 1. 243

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="JA496"

## /db\_xref="taxon:4081"

## /clones="cLEG50N22"

## /tissue\_type="Pericarp"

## /dev stage="breaker"

## /lab\_host="SOLR"

## /clone\_lib="tomato breaker fruit"

## /notes="Vector: pBluescriptSKMcuAdapt; Site 1: EcoRI;

## Site 2: XhoI; supplier: Boyce Thompson Institute;

## sequencing: The Institute for Genomic Research. Fruit

## were harvested at the breaker stage (first sign of

## lycopene accumulation on the blossom end of fruit). Fruit

## were cut in half and the seeds and locules were discarded

## prior to freezing the pericarp."

## ORIGIN

## BM409971

## EST584298

## tomato breaker fruit

## Lycopersicon esculentum

## cLEG50N22

## 5' end, mRNA sequence.

## BM409971.1

## GI:18261601

## Lycopersicon esculentum

## Lycopersicon esculentum

## Sukaryota; Viridiplantae;

## Spermatophyta; Magnoliophyta;

## asterids; lamiales; Solanales;

## Solanaceae; Solanum; Lycopersicon.

## 1 (bases 1 to 243)

## Alcala, J., Vrebalov, J., White, R., Vision, T., Karanymcheva, S.A.,

## Tsai, J., Bongri, O., Kirkness, E., Utterback, T., Van Aken, S.,

## Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

## Giovannoni, J.

## Generation of ESTs from tomato fruit tissue, breaker stage (2002)

## Unpublished (2002)

## Contact: CUGI

## Clemson University

## 100 Jordan Hall, Clemson, SC 29634, USA

## Email: http://www.genome.clemson.edu/orders/index.html

## This clone is available through the Clemson University Genomics

## Institute

## Seq primer: T3.

## Location/Qualifiers

## 1. 243

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="JA496"

## /db\_xref="taxon:4081"

## /clones="cLEG50N22"

## /tissue\_type="Pericarp"

## /dev stage="breaker"

## /lab\_host="SOLR"

## /clone\_lib="tomato breaker fruit"

## /notes="Vector: pBluescriptSKMcuAdapt; Site 1: EcoRI;

## Site 2: XhoI; supplier: Boyce Thompson Institute;

## sequencing: The Institute for Genomic Research. Fruit

## were harvested at the breaker stage (first sign of

## lycopene accumulation on the blossom end of fruit). Fruit

## were cut in half and the seeds and locules were discarded

## prior to freezing the pericarp."

## ORIGIN

## BM409971

## EST584298

## tomato breaker fruit

## Lycopersicon esculentum

## cLEG50N22

## 5' end, mRNA sequence.

## BM409971.1

## GI:18261601

## Lycopersicon esculentum

## Lycopersicon esculentum

## Sukaryota; Viridiplantae;

## Spermatophyta; Magnoliophyta;

## asterids; lamiales; Solanales;

## Solanaceae; Solanum; Lycopersicon.

## 1 (bases 1 to 243)

## Alcala, J., Vrebalov, J., White, R., Vision, T., Karanymcheva, S.A.,

## Tsai, J., Bongri, O., Kirkness, E., Utterback, T., Van Aken, S.,

## Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

## Giovannoni, J.

## Generation of ESTs from tomato fruit tissue, breaker stage (2002)

## Unpublished (2002)

## Contact: CUGI

## Clemson University

## 100 Jordan Hall, Clemson, SC 29634, USA

## Email: http://www.genome.clemson.edu/orders/index.html

## This clone is available through the Clemson University Genomics

## Institute

## Seq primer: T3.

## Location/Qualifiers

## 1. 243

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="JA496"

## /db\_xref="taxon:4081"

## /clones="cLEG50N22"

## /tissue\_type="Pericarp"

## /dev stage="breaker"

## /lab\_host="SOLR"

## /clone\_lib="tomato breaker fruit"

## /notes="Vector: pBluescriptSKMcuAdapt; Site 1: EcoRI;

## Site 2: XhoI; supplier: Boyce Thompson Institute;

## sequencing: The Institute for Genomic Research. Fruit

## were harvested at the breaker stage (first sign of

## lycopene accumulation on the blossom end of fruit). Fruit

## were cut in half and the seeds and locules were discarded

## prior to freezing the pericarp."

## ORIGIN

## BM409971

## EST584298

## tomato breaker fruit

## Lycopersicon esculentum

## cLEG50N22

## 5' end, mRNA sequence.

## BM409971.1

## GI:18261601

## Lycopersicon esculentum

## Lycopersicon esculentum

## Sukaryota; Viridiplantae;

## Spermatophyta; Magnoliophyta;

## asterids; lamiales; Solanales;

## Solanaceae; Solanum; Lycopersicon.

## 1 (bases 1 to 243)

## Alcala, J., Vrebalov, J., White, R., Vision, T., Karanymcheva, S.A.,

## Tsai, J., Bongri, O., Kirkness, E., Utterback, T., Van Aken, S.,

## Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

## Giovannoni, J.

## Generation of ESTs from tomato fruit tissue, breaker stage (2002)

## Unpublished (2002)

## Contact: CUGI

## Clemson University

## 100 Jordan Hall, Clemson, SC 29634, USA

## Email: http://www.genome.clemson.edu/orders/index.html

## This clone is available through the Clemson University Genomics

## Institute

## Seq primer: T3.

## Location/Qualifiers

## 1. 243

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="JA496"

## /db\_xref="taxon:4081"

## /clones="cLEG50N22"

## /tissue\_type="Pericarp"

## /dev stage="breaker"

## /lab\_host="SOLR"

## /clone\_lib="tomato breaker fruit"

## /notes="Vector: pBluescriptSKMcuAdapt; Site 1: EcoRI;

## Site 2: XhoI; supplier: Boyce Thompson Institute;

## sequencing: The Institute for Genomic Research. Fruit

## were harvested at the breaker stage (first sign of

## lycopene accumulation on the blossom end of fruit). Fruit

## were cut in half and the seeds and locules were discarded

## prior to freezing the pericarp."

## ORIGIN

## BM409971

## EST584298

## tomato breaker fruit

## Lycopersicon esculentum

## cLEG50N22

## 5' end, mRNA sequence.

## BM409971.1

## GI:18261601

## Lycopersicon esculentum

## Lycopersicon esculentum

## Sukaryota; Viridiplantae;

## Spermatophyta; Magnoliophyta;

## asterids; lamiales; Solanales;

## Solanaceae; Solanum; Lycopersicon.

## 1 (bases 1 to 243)

## Alcala, J., Vrebalov, J., White, R., Vision, T., Karanymcheva, S.A.,

## Tsai, J., Bongri, O., Kirkness, E

Query Match 100.0%; Score 18; DB 4; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
 |||||  
 Db 24 GGTCTCCATCTCCGATTC 41

RESULT 2  
 AW247015/c  
 LOCUS  
 DEFINITION 279 bp mRNA linear EST 07-JAN-2000  
 2822471.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822471 5',  
 mRNA sequence.  
 ACCESSION AW247015  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 1 (bases 1 to 279)  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other\_ESTs: 2822471.3prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (ILUMI) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/ILUMI at:  
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-I identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu  
 Plate: L1CM9 row: H column: 24  
 High quality sequence stop: 199.

FEATURES  
 source  
 1..279  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2822471"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC.7"  
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5',  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
 Query Match 100.0%; Score 18; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
 |||||  
 Db 197 GGTCTCCATCTCCGATTC 180

RESULT 3  
 AZ576742

LOCUS  
 DEFINITION 344 bp DNA linear GSS 06-DEC-2000  
 AST-2T00919 Genetrapp T47D Human Breast Carcinoma Library Homo  
 sapiens genomic 5', genomic survey sequence.  
 ACCESSION AZ576742  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 1 (bases 1 to 344)  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,  
 Bernardino,A., Durick,K. and Pollok,B.  
 TITLE Exon-trap tags from a T47D GenomesScreen(TM) Library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Greg Henkel  
 Gene Expression  
 Aurora Biosciences Corp.  
 11010 Torreyana Road, San Diego, CA 92121, USA  
 Tel: 8584048436  
 Fax: 8584046719  
 Email: henkel@aurorabio.com  
 Pools of cells were isolated from a GenomesScreen(TM) library. The  
 library of cells was generated by retroviral integration of a gene  
 tagging element consisting of: 1) A promoterless beta-lactamase  
 proceeded by a splice acceptor as a reporter for gene expression;  
 2) A promoter driving neomycin resistance followed by a splice  
 donor to trap downstream exons. 3' RACE from neomycin gene was  
 performed using total RNA from isolated pools. Output was shotgun  
 cloned in pAMP-1 and used to transform DH5-alpha competent  
 bacteria. 5' ends of reported sequences were immediately preceded  
 by splice donor from the trapping construct.  
 Class: exon-trapped.

FEATURES  
 source  
 1..344  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="Carcinoma"  
 /cell\_type="Epithelial"  
 /cell\_line="T47D"  
 /clone\_lib="Genetrapp T47D Human Breast Carcinoma Library"  
 /note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA  
 from genetrapp pools; shotgun clone in pAMP-1 and used to  
 transform DH5-alpha competent bacteria."

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCCATCTCCGATTC 18  
 |||||  
 Db 303 GGTCTCCATCTCCGATTC 320

RESULT 4  
 BM855440/c  
 LOCUS  
 DEFINITION 382 bp mRNA linear EST 06-MAR-2002  
 K-EST0138319 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-67-G02 5',  
 mRNA sequence.  
 ACCESSION BM855440  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 1 (bases 1 to 382)  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001

JOURNAL  
COMMENT

Unpublished (2002)

Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 67 row: G column: 02  
High quality sequence stop: 382.

## FEATURES

source

```
1. 382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-67-G02"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/clone_lib="S21SNU520"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
```

## ORIGIN

```
Query Match 100.0%; Score 18; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGTCTCCATCTCCGATTC 18

|||||

Db 377 GGTCTCCATCTCCGATTC 360

## RESULT 5

AW933481

LOCUS

```
DEFINITION EST359240 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF53L24 5', mRNA sequence.
```

ACCESSION AW933481

VERSION AW933481.1

KEYWORDS GI:8108798

SOURCE EST.

ORGANISM

Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 408)

Alcala, J., Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., and Ronning, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.

Generation of ESTs from tomato fruit tissue

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

## FEATURES

source

Location/Qualifiers

```
1. 408
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF53L24"
/tissue_type="fruit pericarp"
/dev stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
```

## ORIGIN

```
Query Match 100.0%; Score 18; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGTCTCCATCTCCGATTC 18

|||||

Db 67 GGTCTCCATCTCCGATTC 84

## RESULT 6

BM844286/c

LOCUS

```
DEFINITION K-EST0123378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
mRNA sequence.
```

ACCESSION BM844286

VERSION BM844286.1

KEYWORDS GI:19200695

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 63 row: B column: 03

High quality sequence stop: 421.

## FEATURES

source

Location/Qualifiers

```
1. 421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S12SNU216-63-B03"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"
/lab_host="Top10F"
/clone_lib="S12SNU216"
/notes="Organ: Stomach; Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped
```

intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10<sup>+</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18  
 |||||  
 Db 144 GGTCCTCATCTCCGATTC 127

## RESULT 7

CF145335/c  
 LOCUS  
 DEFINITION

CF145335  
 IMAGE:30569057 5', mRNA sequence.

CF145335.1 GI:33260779

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Tim Ratliff

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/humanfl.html

Seq primer: pYX-5.

Location/Qualifiers

1. 421

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30569057"

/tissue\_type="CNCAP(3)/T-225 cell line"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_MGC\_210"

/notes="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoRI;

Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoRI adaptor, digested with Not I and then cloned

directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18  
 |||||  
 Db 138 GGTCCTCATCTCCGATTC 121

## RESULT 8

AW930419

LOCUS

DEFINITION

AW930419

CDNA clone CLEF42D3 5', mRNA sequence.

AW930419

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: CUGI

Unpublished (1999)

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1. 453

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CLEF42D3"

/tissue\_type="fruit pericarp"

/dev\_stage="mature green (3-5 days pre-ripening)"

/lab\_host="SOLR"

/clone\_lib="tomato fruit mature green, TAMU"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:

XhoI; cLEF - Fruit were tagged at the 1cm stage and

harvested 3-5 days prior to ripening. Fruit were cut in

half to verify the seeds were indeed 'immature' and the

seeds and locules were discarded prior to freezing the

pericarp"

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCTCATCTCCGATTC 18

|||||

Db 94 GGTCCTCATCTCCGATTC 111

## RESULT 9

AI777656

LOCUS

DEFINITION

AI777656

EST258451 tomato susceptible, Cornell Lycopersicon esculentum cDNA

clone cLES2M16, mRNA sequence.

455 bp mRNA linear EST 18-MAY-2001

ACCESSION AI777656  
 VERSION AI777656.1 GI:5275613  
 KEYWORDS EST.  
 SOURCE Lycopersicon esculentum (tomato)  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
 1 (bases 1 to 455)  
 D' Ascenzi, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,  
 Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,  
 Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,  
 Giovannoni, J.J. and Martin, G.B.  
 Generation of ESTs from *Pseudomonas* susceptible tomato  
 Contact: CUGI  
 Unpublished (1999)  
 Title  
 JOURNAL  
 COMMENT

FEATURES  
 source

1. 455  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="R11-13 (Rio Grande x Money Maker)"  
 /db\_xref="taxon:4081"  
 /clone="CL52M16"  
 /tissue\_type="leaf"  
 /dev\_stage="4-week old"  
 /lab\_host="SOUR"  
 /clone\_lib="tomato susceptible, Cornell"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; cLES - Tomato *Pseudomonas* Susceptible EST Library.  
 Directionally cloned cDNAs inserted into pBluescript  
 SK(-) at 5' end with EcoRI and 3' end with XhoI site"

## ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTCTCCATCTCCGATTC 18  
 Db 100 GGTCTCCATCTCCGATTC 117

RESULT 10  
 CN422261/c  
 LOCUS CN422261 474 bp mRNA linear EST 16-MAY-2004  
 DEFINITION 17000424524125 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
 ACCESSION CN422261  
 VERSION CN422261.1 GI:47409855  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 474)  
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
 Lebkowski, J. and Stanton, L.W.  
 Transcriptome characterization elucidates signaling networks that  
 control human ES cell growth and differentiation  
 Nat. Biotechnol. 22 (6), 707-716 (2004)  
 JOURNAL  
 COMMENT Contact: Brandenberger R  
 Regenerative Medicine  
 Geron Corporation  
 230 Constitution Drive, Menlo Park, CA 94025, USA  
 Tel: 650 473 8658  
 Fax: 650 473 7760  
 Email: rbrandenberger@geron.com  
 Insert Length: 474 Std Error: 0.00.

FEATURES  
 source  
 1. 474  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="embryonic stem cells, embryoid bodies  
 derived from H1, H7 and H9 cells"  
 /clone\_lib="GRN\_EB"  
 /note="oligo dt primed, full-length enriched cDNA library  
 from embryoid body outgrowths derived from HES cell lines  
 H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
 conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTCTCCATCTCCGATTC 18  
 Db 199 GGTCTCCATCTCCGATTC 182

## RESULT 11

AI283063/c  
 LOCUS AI283063 503 bp mRNA linear EST 29-JAN-1999  
 DEFINITION qm52c06.x1 Soares placenta 8to9weeks 2NbHP8to9w Homo sapiens cDNA  
 clone IMAGE:1893322 3' similar to SW:BCIX\_HUMAN Q07817 APOPTOSIS  
 REGULATOR BCL-X., mRNA sequence.  
 ACCESSION AI283063  
 VERSION AI283063.1 GI:3921296  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 503)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1323 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 440.

## FEATURES

source  
 1. 503  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1893322"  
 /dev\_stage="two placentae: one from 8 weeks and another  
 from 9 weeks post conception"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_placenta 8to9weeks 2NbHP8to9w"  
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3',  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified p773 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M.Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  GGTCCTCATCTCCGATTC 18
Db      494  GGTCCTCATCTCCGATTC 477

RESULT 12
BM857244/c
LOCUS   BM857244               503 bp  mRNA  linear  EST 06-MAR-2002
DEFINITION K-EST0141477 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-78-F09 5', mRNA sequence.
ACCESSION BM857244
VERSION   BM857244.1  GI:19213643
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
          Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
          Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
          Genome Research Center
          Korea Research Institute of Bioscience & Biotechnology
          52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
          Tel: +82-42-860-4470
          Fax: +82-42-860-4409
          Email: yongsung@mail.kribb.re.kr
          Plate: 78 row: F column: 09
          High quality sequence stop: 503.
FEATURES             source
     1..503
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="S21SNUS20-78-F09"
     /sex="F"
     /tissue_types="Stomach"
     /cell_type="Floating aggregates"
     /cell_line="SNU-520"
     /lab_host="Top10F'"
     /clone_lib="S21SNUS20"
     /notes="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
     bacterial alkaline phosphatase (BAP) and then decapped
     with tabacco acid pyrophosphatase (TAP). The decapped
     intact mRNA was ligated with DNA-RNA linker including EcoR
     I site by treatment of T4 RNA ligase and the first strand
     cDNA was synthesized from oligo dt-selected mRNA by
     priming with dt-tailed vector. The dt-tailed vector was
     adjusted to have about 60nt. The cDNA vector was
     circularized with E. coli DNA ligase after digestion of
     EcoRI which site is also included in vector. An RNA strand
     converted to a DNA strand by Okayama-Berg method. The
     obtained cDNA vectors were used for transformation of
     competent cells E. coli Top10F' by electroporation method.
     The cDNA libraries constructed by this method are
     full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTCCTCATCTCCGATTC 18
Db      145  GGTCCTCATCTCCGATTC 128

RESULT 14
CD675630/c
LOCUS   CD675630               560 bp  mRNA  linear  EST 24-JUN-2003
DEFINITION fs2Sh07.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone
          fs2Sh07 5', mRNA sequence.
ACCESSION CD675630
VERSION   CD675630.1  GI:32177361
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS   Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
          Bouffard,G., Smith,D. and Peterson,K.
          Expressed sequence tag analysis of adult human lens for the NEIBank
          Project: over 2000 non-redundant transcripts, novel genes and
          splice variants
          Mol. Vis. 8 (4), 171-184 (2002)
JOURNAL   12103463
MEDLINE   12107413
PUBMED
COMMENT   Contact: Wistow G
          Section on Molecular Structure and Function
          National Eye Institute
          6/331, NIH, Bethesda, MD 20892-2740, USA
          Tel: 301 402 3452

```

Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 25 row: h column: 07  
 Seq primer: M13RP1 reverse primer (ABI)  
 Location/Qualifiers

# FEATURES

source

```
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs25h07"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."
```

# ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 GGCTCCCATCTCCGATTC 18
|||||
Db 370 GGCTCCCATCTCCGATTC 353
```

# RESULT 15

AW931273  
 LOCUS AW931273 571 bp mRNA linear EST 18-MAY-2001  
 DEFINITION EST357116 tomato fruit mature green, TAMU Lycopersicon esculentum  
 cDNA clone CLEF44F15 5', mRNA sequence.

# ACCESSION

AW931273

# VERSION

AW931273.1 GI:8106674

# KEYWORDS

EST

# SOURCE

Lycopersicon esculentum (tomato)

# ORGANISM

Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
 1 (bases 1 to 571)  
 Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Holt, J.E., Liang, F.,  
 Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,  
 Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and  
 Giovannoni, J.

# TITLE

Generation of ESTs from tomato fruit tissue

# JOURNAL

Unpublished (1999)

# COMMENT

Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

# FEATURES

source

```
Location/Qualifiers
1..571
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEF44F15"
/tissue_type="fruit pericarp"
```

```
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  

XhoI; cLEP - Fruit were tagged at the 1cm stage and  

harvested 3-5 days prior to ripening. Fruit were cut in  

half to verify the seeds were indeed 'immature' and the  

seeds and locules were discarded prior to freezing the  

pericarp"
```

# ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 571;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 GGCTCCCATCTCCGATTC 18
|||||
Db 104 GGCTCCCATCTCCGATTC 121
```

Search completed: February 5, 2005, 08:11:49  
 Job time : 2147.2 secs

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-10  
Perfect score: 18  
Sequence: 1 cctgggggtgatgtggagc 18  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	6	BD235158
2	18	100.0	18	6	BD235177
3	18	100.0	391	4	AF245495
4	18	100.0	512	6	CQ272769
5	18	100.0	541	4	AF245487
6	18	100.0	541	4	AF245488
7	18	100.0	541	4	AF245489
8	18	100.0	555	6	CQ113695
9	18	100.0	555	6	CQ152574
10	18	100.0	555	6	CQ185831
11	18	100.0	555	6	CQ235904
12	18	100.0	555	6	CQ273477
13	18	100.0	555	6	CQ310858
14	18	100.0	555	6	CQ347773
15	18	100.0	600	6	CQ100639
16	18	100.0	600	6	CQ139631
17	18	100.0	600	6	CQ175964
18	18	100.0	600	6	CQ222999
19	18	100.0	600	6	CQ260961

20	18	100.0	600	6	CQ298444
21	18	100.0	600	6	CQ335104
22	18	100.0	636	6	BD097037
23	18	100.0	702	4	AY005131
24	18	100.0	702	6	BD084108
25	18	100.0	702	6	BD102202
26	18	100.0	702	9	BT007208
27	18	100.0	702	12	BT008248
28	18	100.0	720	4	AF216205
29	18	100.0	723	9	HSU72398
30	18	100.0	737	6	AR054022
31	18	100.0	737	6	AR172595
32	18	100.0	737	6	IS2012
33	18	100.0	737	6	AR371662
34	18	100.0	737	6	AR380913
35	18	100.0	737	9	HSBCLXS
36	18	100.0	747	6	AX127722
37	18	100.0	752	4	SSJ001203
38	18	100.0	766	4	AF164517
39	18	100.0	926	6	AR054021
40	18	100.0	926	6	AR118504
41	18	100.0	926	6	AR124952
42	18	100.0	926	6	AR144311
43	18	100.0	926	6	AR172594
44	18	100.0	926	6	BD243042
45	18	100.0	926	6	CQ765842

ALIGNMENTS

RESULT 1	BD235158	18 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD235158	18 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Oligonucleotide inhibitors of bcl-xL.				
ACCESSION	BD235158				
VERSION	JP 2002519048-A/10.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Stein, C.A.				
TITLE	Oligonucleotide inhibitors of bcl-xL				
JOURNAL	Patent: JP 2002519048-A 10 02-JUL-2002;				
COMMENT	THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK				
	OS Artificial Sequence				
	PN JP 2002519048-A/10				
	PD 02-JUL-2002				
	PF 02-JUL-1999 JP 2000557839				
	PR 02-JUL-1998 US 09/109614				
	PI CY A STEIN				
	PC				
	C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC				
	A61K47/42,				
	PC A61K47/48, A61K48/00, A61P35/00, C12N15/00				
	CC ANTISENSE OLIGONUCLEOTIDE				
	EH Key Location/Qualifiers				
	FT source 1..18				
	FT Location/Qualifiers				
	1..18				
	/organism="Artificial Sequence".				
	source				
	1..18				
	/organism="synthetic construct"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
	ORIGIN				
	Query Match 100.0%; Score 18; DB 6; Length 18;				
	Best Local Similarity 100.0%; Pred. No. 1.8e+02;				
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
	QY 1 CCTGGGGTGTATGTGGAGC 18				



AUTHORS Amills, M. and Bouzat, J.  
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES  
 source  
 1..541  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="1.1"  
 <1..>541  
 /codon\_start=1  
 /product="anti-apoptotic regulator Bcl-xL"  
 /protein\_id="AAK31306.1"  
 /db\_xref="GI:13591636"  
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG  
 DEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNELFRDGVNWGRIVAFSPFGALCV  
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF  
 NRWFLTGMTVAGVVLGSLF"

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18  
 |||||  
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 6  
 AF245488/c  
 LOCUS Bos taurus clone 1.2 anti-apoptotic regulator Bcl-xL mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF245488.1 GI:13591637  
 VERSION  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES  
 source  
 1..541  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="1.2"  
 <1..>541  
 /codon\_start=1  
 /product="anti-apoptotic regulator Bcl-xL"  
 /protein\_id="AAK31307.1"  
 /db\_xref="GI:13591638"  
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG  
 DEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNELFRDGVNWGRIVAFSPFGALCV  
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF  
 NRWFLTGMTVAGVVLGSLF"

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18  
 |||||  
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 7  
 AF245489/c  
 LOCUS Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF245489.1 GI:13591639  
 VERSION  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES  
 source  
 1..541  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="1.3"  
 <1..>541  
 /codon\_start=1  
 /product="anti-apoptotic regulator Bcl-xL"  
 /protein\_id="AAK31308.1"  
 /db\_xref="GI:13591640"  
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG  
 DEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNELFRDGVNWGRIVAFSPFGALCV  
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF  
 NRWFLTGMTVAGVVLGSLF"

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18  
 |||||  
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 8  
 CQ113695  
 LOCUS Sequence 22554 from Patent WO0157272.  
 DEFINITION  
 ACCESSION CQ113695  
 VERSION CQ113695.1 GI:41083565  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18  
 |||||  
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 7  
 AF245489/c  
 LOCUS Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF245489.1 GI:13591639  
 VERSION  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Characterization of the bovine bcl-xL gene and related pseudogenes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Amills, M. and Bouzat, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAR-2000) Unitat de Genetica, Facultat de Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B., Bellaterra, Barcelona 08193, Spain

FEATURES  
 source  
 1..541  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone="1.3"  
 <1..>541  
 /codon\_start=1  
 /product="anti-apoptotic regulator Bcl-xL"  
 /protein\_id="AAK31308.1"  
 /db\_xref="GI:13591640"  
 /translation="INGNPSWHLADSPAVNGATGHSRSSDAREVIPMAAVKQALREAG  
 DEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNELFRDGVNWGRIVAFSPFGALCV  
 ESDVKEMQVLVSRIATWMATYLNHLEPWIQENGWDTFVELYGNNAAESRKQERF  
 NRWFLTGMTVAGVVLGSLF"

ORIGIN  
 Query Match 100.0%; Score 18; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGTGATGTGGAGC 18  
 |||||  
 Db 200 CCTGGGTGATGTGGAGC 183

RESULT 8  
 CQ113695  
 LOCUS Sequence 22554 from Patent WO0157272.  
 DEFINITION  
 ACCESSION CQ113695  
 VERSION CQ113695.1 GI:41083565  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta  
**JOURNAL** Patent: WO 0157272-A 22554 09-AUG-2001; Aeomica, Inc. (US)

**FEATURES**  
source  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE 0.00e+00"

**ORIGIN**

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 215 CCTGGGGTGATGTGGAGC 232

**RESULT 9**  
CQ152574  
LOCUS CQ152574 555 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 22596 from Patent WO0157276.  
ACCESSION CQ152574  
VERSION CQ152574.1 GI:41159924  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
**AUTHORS** Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow  
**JOURNAL** Patent: WO 0157276-A 22596 09-AUG-2001; Aeomica, Inc. (US)

**FEATURES**  
source  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 4.7-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE 0.00e+00"

**ORIGIN**

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 215 CCTGGGGTGATGTGGAGC 232

**RESULT 10**  
CQ185831  
LOCUS CQ185831 555 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 17227 from Patent WO0157274.  
ACCESSION CQ185831  
VERSION CQ185831.1 GI:41180846  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
1

**AUTHORS** Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart  
**JOURNAL** Patent: WO 0157274-A 17227 09-AUG-2001; Aeomica, Inc. (US)

**FEATURES**  
source  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.4-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE 0.00e+00"

**ORIGIN**

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 215 CCTGGGGTGATGTGGAGC 232

**RESULT 11**  
CQ235904  
LOCUS CQ235904 555 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 22743 from Patent WO0157273.  
ACCESSION CQ235904  
VERSION CQ235904.1 GI:41219182  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
**AUTHORS** Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
**TITLE** HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263,6<151> 03 October 2000 (27.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine  
**JOURNAL** Patent: WO 0157273-A 22743 09-AUG-2001; Aeomica, Inc. (US)

**FEATURES**  
source  
Location/Qualifiers  
1..555  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL = 1.7-SWISSPROT HIT: Q07817, EVALUATE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUATE 0.00e+00-NT HIT: U72398.1, EVALUATE 0.00e+00"

**ORIGIN**

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 215 CCTGGGGTGATGTGGAGC 232

**RESULT 12**  
CQ273477  
LOCUS CQ273477 555 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 21738 from Patent WO0157277.

```

ACCESSION      CQ273477
VERSION        CQ273477.1  GI:41246081
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 21738 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..555
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
              HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
              0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 13
CQ310858
LOCUS      CQ310858          555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21963 from Patent WO0186003.
ACCESSION  CQ310858
VERSION    CQ310858.1  GI:41271435
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human lung
JOURNAL   Patent: WO 0186003-A 21963 15-NOV-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
          source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
          2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
          BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
          0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 14
CQ347773
LOCUS      CQ347773          555 bp      DNA      linear      PAT 23-JAN-2004
DEFINITION Sequence 21867 from Patent WO0157275.
ACCESSION  CQ347773
VERSION    CQ347773.1  GI:41296844
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human brain
JOURNAL   Patent: WO 0157275-A 21867 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
          source
            1..555
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
          1.6-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT:
          BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
          0.00e+00"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      215 CCTGGGGTGATGTGGAGC 232

RESULT 15
CQ100639
LOCUS      CQ100639          600 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 9498 from Patent WO0157272.
ACCESSION  CQ100639
VERSION    CQ100639.1  GI:41069665
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
          analysis of gene expression in human placenta
JOURNAL   Patent: WO 0157272-A 9498 09-AUG-2001;
          Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
          source
            1..600
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
          0.99"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGGGTGATGTGGAGC 18
        |||||
Db      234 CCTGGGGTGATGTGGAGC 251

Search completed: February 4, 2005, 23:30:41
Job time : 432.664 secs

```

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169a-10  
Perfect score: 18  
Sequence: 1 cctggggtgatgtggagc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46980 Bcl-X1 mr
2	18	100.0	555	4	Aba73433 Human foe
3	18	100.0	555	4	Aa153868 Probe #22
4	18	100.0	555	4	Aba38761 Probe #17
5	18	100.0	555	4	Aak48039 Human bon
6	18	100.0	555	4	Aak21876 Human bra
7	18	100.0	555	4	Abs47753 Human liv
8	18	100.0	555	4	Abs21972 Human gen
9	18	100.0	564	12	Ach87595 Human gen
10	18	100.0	600	4	Aba60917 Human foe
11	18	100.0	600	4	Aa140812 Probe #94
12	18	100.0	600	4	Aba28894 Probe #73
13	18	100.0	600	4	Aak35096 Human bon
14	18	100.0	600	4	Aak09207 Human bra
15	18	100.0	600	4	Abs34848 Human liv
16	18	100.0	600	6	Abs09558 Human gen
17	18	100.0	636	4	Aah48169 Mutant bc
18	18	100.0	702	5	Aah43464 cDNA clon
19	18	100.0	702	12	Adm45994 Human apo
20	18	100.0	737	2	Aa81699 Human thy
21	18	100.0	737	10	Abz83507 Toxicology

c	22	18	100.0	737	11	ADI32132	Adi32132 Human cdn
c	23	18	100.0	739	12	ADG65218	Adg65218 Human bcl
c	24	18	100.0	747	4	AAF30926	Aaf30926 Human bcl
c	25	18	100.0	747	12	ADG65209	Adg65209 Human bcl
c	26	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
c	27	18	100.0	926	2	AA740079	Aat40079 Bcl-XL ge
c	28	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
c	29	18	100.0	926	4	AAAS15189	Aas15189 Human bcl
c	30	18	100.0	926	4	AAC90810	Aac90810 Human bcl
c	31	18	100.0	926	6	ABK84766	Abk84766 Human cdn
c	32	18	100.0	926	8	ABTI6641	Abt16641 Human bcl
c	33	18	100.0	926	10	ADD56779	Add56779 Human bcl
c	34	18	100.0	926	10	ADG64187	Adg64187 Human bcl
c	35	18	100.0	926	11	ADI32104	Adi32104 Human cdn
c	36	18	100.0	926	12	ADH52630	Adh52630 Human ant
c	37	18	100.0	926	12	ADQ19990	Ado19990 Human PRO
c	38	18	100.0	926	12	ADP13351	Adp13351 Renal cel
c	39	18	100.0	1216	5	AAS00247	Aas00247 Bcl-X1-DT
c	40	18	100.0	1455	5	AAS00250	Aas00250 LFn-Bcl-X
c	41	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
c	42	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
c	43	18	100.0	2575	12	ADQ19866	Ado19866 Human PRO
c	44	18	100.0	7372	2	AAX33182	Aax33182 Base sequ
c	45	16.4	91.1	492	9	ACH46093	Ach46093 Human inf

ALIGNMENTS

RESULT 1  
AAZ46980  
ID AAZ46980 standard; DNA; 18 BP.  
XX  
AC AAZ46980;  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-X1 mRNA specific antisense oligo J.  
XX  
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Stein CA;  
XX  
DR WPI; 2000-137140/12.  
XX  
PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-  
PT xL, useful for reducing bcl-xL production in tumor cells to treat cancer  
PT or in vascular cells to promote the regression of vascular lesions.  
XX  
PS Claim 1; Fig 1; 69pp; English.  
XX  
CC The invention provides antisense oligonucleotides or their derivatives  
CC which reduce or eliminate expression of the anti-apoptotic protein bcl-  
CC xL. The oligonucleotides can be introduced into tumour cells to reduce  
CC bcl-xL production to treat cancer, especially epithelial cancer, e.g.  
CC prostate, lung or bladder cancer. Oligonucleotides comprising one or more  
CC bases with a C-5 propynyl pyrimidine modification may especially be used  
CC to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in  
CC such treatment. The oligonucleotides can be introduced into vascular  
CC cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 2 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18  
 Db 1 CCTGGGGTGATGTGGAGC 18

RESULT 2  
 ABA73433  
 ID ABA73433 standard; DNA; 555 BP.

XX AC ABA73433;

XX DT 01-FEB-2002 (first entry)

XX DE Human foetal liver single exon nucleic acid probe #21738.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 gene expression in human fetal liver.

XX PS Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring  
 human gene expression in a sample derived from human foetal liver. The  
 single exon nucleic acid probes may be used for predicting, measuring and  
 displaying gene expression in samples derived from human fetal liver. The  
 present sequence is a single exon nucleic acid probe of the invention.  
 Note: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18  
 Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 3  
 AAI53868  
 ID AAI53868 standard; DNA; 555 BP.

XX AC AAI53868;

XX DT 17-OCT-2001 (first entry)

XX DE Probe #22554 used to measure gene expression in human placenta sample.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 gene expression in human placenta.

XX PS Claim 25; SEQ ID NO 22554; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP).  
 The present sequence is one such probe. The probes are useful for  
 producing a microarray for predicting, measuring and displaying gene  
 expression in samples derived from human placenta. The probes are useful  
 for antenatal diagnosis of human genetic disorders

XX SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18  
 Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 4  
 ABA38761

ID ABA38761 standard; DNA; 555 BP.

XX AC ABA38761;

XX DT 23-JAN-2002 (first entry)

XX DE Probe #17227 for gene expression analysis in human heart cell sample.

XX KW Human; gene expression; heart; microarray; vascular system; probe;  
 cardiovascular disease; hypertension; cardiac arrhythmia;  
 congenital heart disease; ss.



```
OS Homo sapiens.
XX WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000666.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX Claim 4; SEQ ID NO 17227; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: the sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 4; Length 555;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTGGGGTGATGTGGAGC 18
XX |||||
XX Db 215 CCTGGGGTGATGTGGAGC 232
XX
XX RESULT 5
XX AAK48039
XX ID AAK48039 standard; DNA; 555 BP.
XX AC AAK48039;
XX AC
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 22596.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Query Match 100.0%; Score 18; DB 4; Length 555;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTGGGGTGATGTGGAGC 18
XX |||||
XX Db 215 CCTGGGGTGATGTGGAGC 232
XX
XX RESULT 6
XX AAK21876
XX ID AAK21876 standard; DNA; 555 BP.
XX AC AAK21876;
XX AC
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 21867.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
```

```
XX PS Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX CC
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
Db 215 CCTGGGGTGATGTGGAGC 232
RESULT 7
ID ABS47753 standard; DNA; 555 BP.
XX AC ABS47753;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID No 22743.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX PS Claim 4; SEQ ID NO 22743; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
```

```
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification which was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
SQ Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
Db 215 CCTGGGGTGATGTGGAGC 232
RESULT 8
ID ABS21972 standard; DNA; 555 BP.
XX AC ABS21972;
XX DT 19-AUG-2002 (first entry)
XX DE Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX PD 15-NOV-2001.
XX PF 30-JAN-2001; 2001WO-US0000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX PS Claim 4; SEQ ID NO 21963; 634pp; English.
XX CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
```

mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 555;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGTGGAGC 18  
Db 215 CCTGGGGTGTGGAGC 232

RESULT 9  
ACH87595  
ID ACH87595 standard; DNA; 564 BP.

XX ACH87595;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20790.

XX Human; probe; ss; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

XX gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.

XX Claim 1; SEQ ID NO 20790; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene  
XX expression, comprising any of the 27,400 fully defined nucleotide  
XX sequences in the specification, or their complements or fragments, and  
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences  
XX fully defined in the specification. The probe is a single exon probe that  
XX hybridises under high stringency conditions to a nucleic acid molecule  
XX expressed in human cells or tissues. Also included are a spatially-  
XX addressable set of single exon nucleic acid probes for measuring human  
XX gene expression (comprising a plurality of single exon nucleic acid  
XX probes cited above, where each of the plurality of probes is separately  
XX and addressably isolatable or amplifiable from the plurality), a single  
XX exon microarray for measuring human gene expression, a method of  
XX measuring human gene expression, a vector comprising the single exon  
XX probe cited above, an ORF-encoded peptide comprising at least 8  
XX contiguous amino acids of any of the above-mentioned amino acid  
XX sequences (optionally with conservative amino acid substitutions), an  
XX isolated antibody that binds specifically to a peptide cited above,  
XX methods of selling and/or licensing single exon probes or microarrays to  
XX a customer desiring to measure gene expression, a method of providing  
XX human gene expression data by subscription, and a computer-readable  
XX storage medium which contains a database having a plurality of records  
XX (each record including data on the expression of a single exon probe  
XX cited above). The probe, methods and apparatus are useful in gene  
XX expression analysis. The probes may be used as tools for surveying  
XX tissues to detect the presence of expressed messages that contain their  
XX specific exon, or in constructing genome-derived single exon microarrays.  
XX In addition, the probes are used in identifying and characterising  
XX alternative splicing events, in detecting and characterising gross  
XX alterations in the genomic locus that includes their exon, in assessing  
XX smaller genomic alterations, in priming the synthesis of nucleic acids,  
XX or in expressing the ORF-encoded peptide. The present sequence is a human  
XX single exon probe of the invention. Note: The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from USPTO at  
XX seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 564;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGTGGAGC 18

Db 215 CCTGGGGTGTGGAGC 232

RESULT 10

ABAG0917

ID ABAG0917 standard; DNA; 600 BP.

XX ABAG0917;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #9222.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.



```
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
  Query Match      100.0%; Score 18; DB 4; Length 600;
  Best Local Similarity 100.0%; Pred. No. 65;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 1 CCTGGGGTGATGTGGAGC 18
  Db 234 CCTGGGGTGATGTGGAGC 251

RESULT 13
AAK35096
ID AAK35096 standard; DNA; 600 BP.
XX AC
XX AC AAK35096;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 9653.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488900/53.
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX CC the probes of the invention
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
  Query Match      100.0%; Score 18; DB 4; Length 600;
  Best Local Similarity 100.0%; Pred. No. 65;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 1 CCTGGGGTGATGTGGAGC 18
  Db 234 CCTGGGGTGATGTGGAGC 251

RESULT 14
AAK09207
ID AAK09207 standard; DNA; 600 BP.
XX AC
XX AC AAK09207;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 9198.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-483446/52.
XX XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is one of the probes of the
XX CC invention
XX SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
XX
  Query Match      100.0%; Score 18; DB 4; Length 600;
  Best Local Similarity 100.0%; Pred. No. 65;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 1 CCTGGGGTGATGTGGAGC 18
  Db 234 CCTGGGGTGATGTGGAGC 251

RESULT 15
ABS34848
ID ABS34848 standard; DNA; 600 BP.
XX AC
XX AC ABS34848;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID No 9838.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
XX KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX KW coronary heart disease; ss.
XX OS Homo sapiens.
```

XX WO200157273-A2.  
PN  
XX  
PD  
XX  
PF 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488898/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
PS Claim 1; SEQ ID NO 9838; 658pp; English.  
XX  
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification for complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 600;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTGGGGTGATGTGGAGC 18  
|||  
Db 234 CCTGGGGTGATGTGGAGC 251  
  
Search completed: February 4, 2005, 21:52:43  
Job time : 232.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169a-10  
Perfect score: 18  
Sequence: 1 cctgggggtgatgtggagc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	161	2 BE771987	BE771987 CM3-FT010
2	18	100.0	294	2 BE818722	BE818722 PM3-BN030
3	18	100.0	299	7 F08773	F08773 HSC25B061 n
4	18	100.0	305	4 B1399503	B1399503 MI-P-AY1
5	18	100.0	310	4 B1060608	B1060608 IL3-UT011
6	18	100.0	344	8 A2576742	A2576742 AST-2T009
7	18	100.0	418	4 B1051278	B1051278 CM3-GN029
8	18	100.0	421	4 BM844286	BM844286 K-EST0122
9	18	100.0	421	6 CF145335	CF145335 UI-HF-CB0
10	18	100.0	437	7 W01420	W01420 za73d06.r1
11	18	100.0	456	8 A2537061	A2537061 AST-2P015
12	18	100.0	474	7 CN422261	CN422261 170004245
13	18	100.0	475	5 BQ331598	BQ331598 MR4-ET013
14	18	100.0	478	4 BM050133	BM050133 6036332480
15	18	100.0	485	2 AW814883	AW814883 MR1-ST020
16	18	100.0	503	4 BM857244	BM857244 K-EST0141
17	18	100.0	516	7 H09884	H09884 ym05b07.r1
18	18	100.0	542	7 CN422262	CN422262 170004245
19	18	100.0	577	6 CF131978	CF131978 UI-HF-F00
20	18	100.0	584	1 AL134785	AL134785 DKFZP547K
21	18	100.0	587	2 BE871836	BE871836 601447837
22	18	100.0	608	4 B1960951	B1960951 MONOL_3A
23	18	100.0	611	6 CB448211	CB448211 702275 MA
24	18	100.0	612	2 BE783664	BE783664 601471247

C 25	18	100.0	632	7 CN422264	CN422264 170005326
C 26	18	100.0	657	2 BE207063	BE207063 ba09f05.Y
C 27	18	100.0	671	2 AW814739	AW814739 MRI-ST020
C 28	18	100.0	675	7 CK832794	CK832794 4056483 B
C 29	18	100.0	687	2 BE293685	BE293685 601186941
C 30	18	100.0	698	4 BG708652	BG708652 602672575
C 31	18	100.0	697	4 B1457116	B1457116 603183360
C 32	18	100.0	699	2 BE870269	BE870269 601447403
C 33	18	100.0	700	4 BG831301	BG831301 602766132
C 34	18	100.0	704	4 B1561500	B1561500 603256193
C 35	18	100.0	705	4 BG290422	BG290422 602388270
C 36	18	100.0	707	6 CD636467	CD636467 56049107H
C 37	18	100.0	714	4 BG470667	BG470667 602511594
C 38	18	100.0	716	7 CK317449	CK317449 SB02021A2
C 39	18	100.0	720	6 CD636470	CD636470 56049223J
C 40	18	100.0	735	6 CD641746	CD641746 AGENCOURT
C 41	18	100.0	765	2 BF569393	BF569393 602185659
C 42	18	100.0	782	2 BE249973	BE249973 600943141
C 43	18	100.0	798	5 BQ687097	BQ687097 AGENCOURT
C 44	18	100.0	798	5 B0528551	B0528551 AGENCOURT
C 45	18	100.0	798	7 CK000319	CK000319 AGENCOURT

## ALIGNMENTS

RESULT 1  
BE771987  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BE771987 161 bp mRNA linear EST 20-SEP-2000  
CM3-FT0100-140700-245-e05 FT0100 Homo sapiens cDNA, mRNA sequence.  
BE771987  
BE771987.1 GI:10225645  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 161)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-cw3-FT0100-140  
700-245-e05&t3=2000-07-14&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 69.

FEATURES  
source

Location/Qualifiers  
1..161  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="FT0100"  
/notes="Organ: prostate tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 107 CCTGGGGTGATGTGGAGC 124

## RESULT 2

BE818722/c  
LOCUS 294 bp mRNA linear EST 21-SEP-2000  
DEFINITION PM3-BN0300-080700-002-g11 BN0300 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE818722  
VERSION BE818722.1 GI:10250956  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS 1 (bases 1 to 294)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## MEDLINE

20202663

## PUBMED

10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tit=&t2=PM3-BN0300-080700-002-g11&t3=2000-07-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 33

High quality sequence stop: 294.

## FEATURES

## source

1..294  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BN0300"  
/note="Organ: breast normal; Vector: puc18; Site\_1: Smal; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 294;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
|||||  
Db 190 CCTGGGGTGATGTGGAGC 173

## RESULT 3

## F08773/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY

## Db

## RESULT 4

## BI399503

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## QY



```

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 305)
Bonald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: Tugle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ctugle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone Distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=No.

Location/Qualifiers
1..305
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clones="MI-P-A11-nrg-c-08-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MI-P-A11"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A11
library is normalized library derived from the MI-P-A10
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)
TAG_SEQ=None found"

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
| | | | | | | | | | | | | | | | | |
Db 215 CCTGGGGTGATGTGGAGC 232

RESULT 5
BI060608
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BI060608 310 bp mRNA linear EST 15-JUN-2001
DEFINITION
IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BI060608
VERSION
BI060608.1 GI:14468135
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 310)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0115-
300101-433-B03&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 310.

FEATURES
source
1..310
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev stage="Adult"
/clone_lib="UT0115"
/notes="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGGGTGATGTGGAGC 18
| | | | | | | | | | | | | | | | | |
Db 94 CCTGGGGTGATGTGGAGC 111

RESULT 6
AZ576742
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ576742 344 bp DNA linear GSS 06-DEC-2000
DEFINITION
AST-2T00919 Genetrap T47D Human Breast Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.
ACCESSION
AZ576742
VERSION
AZ576742.1 GI:11563053
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Bernardino, A., Durick, K. and Pollok, B.
Exon-trap tags from a T47D GenomeScreen(TM) Library
Unpublished (2000)
Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase

```

proceeded by a splice acceptor as a reporter for gene expression;  
 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.  
 Class: exon-trapped.

# FEATURES

source

Location/Qualifiers  
 1. .344  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="Carcinoma"  
 /cell\_type="Epithelial"  
 /cell\_line="T47D"  
 /clone\_lib="Genetrap T47D Human Breast Carcinoma Library"  
 /note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

## ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
 |||||  
 Db 97 CCTGGGGTGATGTGGAGC 114

## RESULT 7

BI051278  
 LOCUS 418 bp mRNA linear EST 15-JUN-2001  
 DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BI051278  
 VERSION BI051278.1 GI:14458808

KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 418)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-110101-607-f03&t3=2001-01-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 3

High quality sequence stop: 418.

## FEATURES

source

Location/Qualifiers  
 1. .418  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
 |||||  
 Db 375 CCTGGGGTGATGTGGAGC 392

## RESULT 8

BM844286/c

LOCUS 421 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5', mRNA sequence.

ACCESSION BM844286

VERSION BM844286.1 GI:19200695

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 421)

## REFERENCE

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 63 row: B column: 03

High quality sequence stop: 421.

## FEATURES

source

Location/Qualifiers  
 1. .421  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S12SNU216-63-B03"  
 /sex="F"  
 /tissue\_type="Lymph node"  
 /cell\_type="Epithelial"  
 /cell\_line="SNU-216"  
 /lab\_host="Top10P"  
 /clone\_lib="S12SNU216"

/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of



```

sapiens genomic 5', genomic survey sequence.
AZ537061
VERSION AZ537061.1 GI:111113828
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Bernardino, A., Durick, K. and Pollok, B.
TITLE Exon-trap tags from a PC-3 GenomeScreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelga@aurabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
preceded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.
FEATURES
source Location/Qualifiers
1..456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
Library"
/notes="Organ: Prostate; Vector: pAMP-1; 3' RACE of total
RNA from genetrap pools; shotgun clone in pAMP-1 and used
to transform DH5-alpha competent bacteria."
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 346 CCTGGGGTGATGTGGAGC 363

RESULT 12
CN422261/c
LOCUS CN422261 474 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424524125 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN422261
VERSION CN422261.1 GI:47409855
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murgue, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 474 Std Error: 0.00.
Location/Qualifiers
1..474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from HL, H7 and H9 cells"
/clone_lib="GRN EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN
Query Match 100.0%; Score 18; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGGGTGATGTGGAGC 18
|||||
Db 408 CCTGGGGTGATGTGGAGC 391

RESULT 13
BQ331598/c
LOCUS BQ331598 475 bp mRNA linear EST 17-MAY-2002
DEFINITION MR4-ET0138-080501-010-d06 ET0138 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ331598
VERSION BQ331598.1 GI:20972765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-ET0138-
080501-010-d06&t3=2001-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence stop: 475.
Location/Qualifiers
1..475
/organism="Homo sapiens"
/mol_type="mRNA"
FEATURES
source

```

/db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="ET0138"  
 /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No.196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 475;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18  
 ||||||||||||  
 Db 242 CCTGGGGTGATGTGGAGC 225

RESULT 14  
 BM050133/c  
 LOCUS  
 DEFINITION 603632480F1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5422338 5',  
 mRNA sequence.

ACCESSION BM050133  
 VERSION BM050133.1 GI:16779400

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 478)

NTN-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Straubeberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM1879 row: p column: 19

High quality sequence stop: 267.

## FEATURES

source

Location/Qualifiers  
 1..478  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="NIH\_MGC 42"  
 /tissue="epithelioid carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC 42"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18

Db 90 CCTGGGGTGATGTGGAGC 73  
 ||||||||||||

## RESULT 15

AW814883

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 486)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR1-ST0206-120

400-022-f04&t3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

## FEATURES

" source

Location/Qualifiers  
 1..486  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="ST0206"  
 /note="Organ: stomach; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No.196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 486;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGGGTGATGTGGAGC 18

||||||||||

Db 339 CCTGGGGTGATGTGGAGC 356

Search completed: February 5, 2005, 08:11:51  
 Job time : 2148.2 secs

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-11

Perfect score: 18  
Sequence: 1 agttccacaaaagtatcc 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_ptg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235159
2	18	100.0	18	6	BD235178
3	18	100.0	18	6	BD235179
4	18	100.0	387	6	CQ732731
5	18	100.0	587	6	CQ099589
6	18	100.0	587	6	CQ138575
7	18	100.0	587	6	CQ175406
8	18	100.0	587	6	CQ221990
9	18	100.0	587	6	CQ259335
10	18	100.0	587	6	CQ297711
11	18	100.0	587	6	CQ334058
12	18	100.0	636	6	BD097037
13	18	100.0	702	6	BD084108
14	18	100.0	702	6	BD102202
15	18	100.0	702	9	BT007208
16	18	100.0	702	12	BT008248
17	18	100.0	737	6	AR054022
18	18	100.0	737	6	AR172595
19	18	100.0	737	6	I52012

c 20	18	100.0	737	6	AR371662
c 21	18	100.0	737	6	AR380913
c 22	18	100.0	737	9	HSBCLXS
c 23	18	100.0	747	6	AX127722
c 24	18	100.0	926	6	AR054021
c 25	18	100.0	926	6	AR118504
c 26	18	100.0	926	6	AR124952
c 27	18	100.0	926	6	AR144311
c 28	18	100.0	926	6	AR172594
c 29	18	100.0	926	6	BD243042
c 30	18	100.0	926	6	CQ765842
c 31	18	100.0	926	6	CQ765842
c 32	18	100.0	926	6	I52011
c 33	18	100.0	926	6	AR371661
c 34	18	100.0	926	6	AR380885
c 35	18	100.0	926	6	AX839772
c 36	18	100.0	926	6	AX925686
c 37	18	100.0	926	9	HSBCLXL
c 38	18	100.0	1163	4	AB080951
c 39	18	100.0	1236	6	AX085490
c 40	18	100.0	1252	4	AB073983
c 41	18	100.0	1455	6	AX085496
c 42	18	100.0	2575	6	CQ827863
c 43	18	100.0	2575	9	BC019307
c 44	18	100.0	7372	6	E23357
c 45	18	100.0	99593	9	HSJ857M17

ALIGNMENTS

BD235159 18 bp DNA linear PAT 17-JUL-2003  
Oligonucleotide inhibitors of bcl-xL.

BD235159 GI:33044929

JP 2002519048-A/11.

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 18)

Stein, C.A.

Oligonucleotide inhibitors of bcl-xL

Patent: JP 2002519048-A 11 02-JUL-2002;

THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

OS Artificial Sequence

PN JP 2002519048-A/11

PD 02-JUL-2002

PF 02-JUL-1999 JP 2000557839

PR 02-JUL-1998 US 09/109614

PI CY A STEIN

PC C12N15/09, A61K9/127, A61K31/711, A61K31/712, A61K31/7125, PC

A61K47/42,

PC A61K47/48, A61K48/00, A61P35/00, C12N15/00

CC ANTISENSE OLIGONUCLEOTIDE

FH Key Location/Qualifiers

FT source 1..18

FT Location/Qualifiers

source 1..18

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

|||||





```

QY 1 AGTTCACAAAAGTATCC 18
Db 266 AGTTCACAAAAGTATCC 249

RESULT 5
LOCUS CO099589
DEFINITION Sequence 8448 from Patent WO0157272.
ACCESSION CO099589
VERSION CQ099589.1 GI:41068615
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 8448 09-AUG-2001;
FEATURES Location/Qualifiers
source 1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 1.5"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 6
LOCUS CQ138575
DEFINITION Sequence 8597 from Patent WO0157276.
ACCESSION CQ138575
VERSION CQ138575.1 GI:41095941
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 8597 09-AUG-2001;
FEATURES Location/Qualifiers
source 1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL = 5.5"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 7
LOCUS CQ175406
DEFINITION Sequence 6802 from Patent WO0157274.
ACCESSION CQ175406
VERSION CQ175406.1 GI:41170145
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 6802 09-AUG-2001;
FEATURES Location/Qualifiers
source 1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.6"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18
Db 510 AGTTCACAAAAGTATCC 527

RESULT 8
LOCUS CQ221990
DEFINITION Sequence 8829 from Patent WO0157273.
ACCESSION CQ221990
VERSION CQ221990.1 GI:41204114
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
JOURNAL Molecular Dynamics Sequence Listing Engine
FEATURES Location/Qualifiers
source 1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL = 1.9"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGTTCACAAAAGTATCC 18
Db      510 AGTTCACAAAAGTATCC 527

RESULT 9
LOCUS   CQ259935
DEFINITION
Sequence 8196 from Patent WO0157277.
ACCESSION CQ259935
VERSION   CQ259935.1 GI:41232415
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE    Human genome-derived single exon nucleic acid probes useful for
JOURNAL  analysis of gene expression in human fetal liver
PATENT:  WO 0157277-A 8196 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
= 4.1"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
Db      510 AGTTCACAAAAGTATCC 527

RESULT 10
LOCUS   CQ297711
DEFINITION
Sequence 8816 from Patent WO0186003.
ACCESSION CQ297711
VERSION   CQ297711.1 GI:41258288
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE    Human genome-derived single exon nucleic acid probes useful for
JOURNAL  analysis of gene expression in human lung
PATENT:  WO 0186003-A 8816 15-NOV-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL = 2.2"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
Db      510 AGTTCACAAAAGTATCC 527

RESULT 11
LOCUS   CQ334058
DEFINITION
Sequence 8152 from Patent WO0157275.
ACCESSION CQ334058
VERSION   CQ334058.1 GI:41283090
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE    Human genome-derived single exon nucleic acid probes useful for
JOURNAL  analysis of gene expression in human brain
PATENT:  WO 0157275-A 8152 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL = 2"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
Db      510 AGTTCACAAAAGTATCC 527

RESULT 12
LOCUS   BD097037/c
DEFINITION
A BH4 fusion polypeptide.
ACCESSION BD097037
VERSION   BD097037.1 GI:22642625
KEYWORDS synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 636)
AUTHORS Shimizu, S. and Tsujimoto, Y.
TITLE    A BH4 fusion polypeptide
JOURNAL  Patent: WO 0148014-A 3 05-JUL-2001;
SHIONOGI & CO LTD, SHIGEMI SHIMIZU, YOSHIHI TSUJIMOTO
COMMENT  OS Artificial Sequence
PN WO 0148014-A/3
PD 05-JUL-2001
PF 26-DEC-2000 WO 2000JP009274
PI 27-DEC-1999 JP 99P 371449
PR SHIGEMI SHIMIZU, YOSHIHI TSUJIMOTO
PC C07K14/47, C12N15/12, A61K38/17, A61P9/10
CC Synthesized DNA for mutant bcl-x L.
FH Key Location/Qualifiers
FT CDS
(1)..(636).
Location/Qualifiers
1..636
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTTCACAAAAGTATCC 18
Db      510 AGTTCACAAAAGTATCC 18

```

## ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 702;  
Best Local Similarity 100.0%; Fred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCACAAAAGTATCC 18  
|||||  
Db 581 AGTTCCACAAAAGTATCC 564

Search completed: February 4, 2005, 23:30:42  
Job time : 433.664 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-11  
Perfect score: 18  
Sequence: 1-agtccacaaagtatccc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46981 Bcl-XL mr
2	18	100.0	179	12	Ach84269 Human gen
3	18	100.0	337	10	Adk66037 Standardi
4	18	100.0	492	9	Ach46093 Human inf
5	18	100.0	587	4	Aba59891 Human foe
6	18	100.0	587	4	Aai39762 Probe #84
7	18	100.0	587	4	Aba28336 Probe #68
8	18	100.0	587	4	Aak34040 Human bon
9	18	100.0	587	4	Aak08161 Human bra
10	18	100.0	587	4	Abs33839 Human liv
11	18	100.0	587	6	Abs08825 Human gen
12	18	100.0	587	12	Ach70569 Human gen
13	18	100.0	636	4	Aah48169 Mutant bc
14	18	100.0	702	5	Aah43464 cDNA clon
15	18	100.0	702	12	Adm45994 Human apo
16	18	100.0	737	2	Arq08169 Human thy
17	18	100.0	737	11	Abz83507 Toxilog
18	18	100.0	737	11	Adi32132 Human cdn
19	18	100.0	739	12	Adg65218 Human bcl
20	18	100.0	747	4	Aaf30926 Human bcl
21	18	100.0	747	12	Adg65209 Human Bcl

c	22	18	100.0	926	2	AAQ81698	Aa81698 Human thy
c	23	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
c	24	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
c	25	18	100.0	926	4	AAS15189	Aas15189 Human bcl
c	26	18	100.0	926	4	AAC90810	Aac90810 Human bcl
c	27	18	100.0	926	6	ABK84766	Abk84766 Human cdn
c	28	18	100.0	926	8	ABT16641	Abt16641 Human bcl
c	29	18	100.0	926	10	ADD56779	Add56779 Human bcl
c	30	18	100.0	926	10	AAD64187	Aad64187 Human bcl
c	31	18	100.0	926	11	ADI32104	Adi32104 Human cdn
c	32	18	100.0	926	12	ADH52630	Adh52630 Human ant
c	33	18	100.0	926	12	ADO19990	Ado19990 Human PRO
c	34	18	100.0	926	12	ADP13351	Adp13351 Renal cel
c	35	18	100.0	1236	5	AAS00247	Aas00247 Bcl-XL-DT
c	36	18	100.0	1455	5	AAS00250	Aas00250 LFN-Bcl-X
c	37	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
c	38	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
c	39	18	100.0	2575	12	ADO19866	Ado19866 Human PRO
c	40	18	100.0	7372	2	AAX33182	Aax33182 Base sequ
	41	17.2	95.6	20	3	AAC65053	Aac65053 Human bcl
	42	17	94.4	20	3	AAZ93647	Aaz93647 Antisense
	43	17	94.4	20	4	AAS15196	Aas15196 Human bcl
	44	17	94.4	20	5	AAB27692	Aab27692 Human bcl
	45	17	94.4	20	6	ABV73654	Abv73654 Human bcl

ALIGNMENTS

RESULT 1  
AAZ46981  
ID AAZ46981 standard; DNA; 18 BP.  
XX AC AAZ46981;  
XX DT 14-APR-2000 (first entry)  
XX DE Bcl-XL mRNA specific antisense oligo K.  
XX KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
XX KM lung; bladder; bcl-2; vascular lesion; antisense; ss.  
XX OS Homo sapiens.  
XX SS WO200001393-A2.  
XX PN 13-JAN-2000.  
XX PD 02-JUL-1999; 99WO-US015250.  
XX PF 02-JUL-1998; 98US-00109614.  
XX PR (UYCO ) UNIV COLUMBIA NEW YORK.  
XX PA Stein CA;  
XX PI WPI; 2000-137140/12.  
XX DR New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
XX PT Claim 1; Fig 1; 69pp; English.  
XX PS The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

Db 1 AGTTCACAAAAGTATCC 18

# RESULT 2

ACH84269/c  
 ID ACH84269 standard; DNA; 179 BP.

XX ACH84269;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #17464.

XX Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.

XX Claim 1; SEQ ID NO 17464; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridizes under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 179;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18

Db 37 AGTTCACAAAAGTATCC 20

# RESULT 3

ADK66037/c

ID ADK66037 standard; DNA; 337 BP.

XX ADK66037;

XX 06-MAY-2004 (first entry)

XX Standardized polynucleotide system polynucleotide #8.

XX ss; standardized polynucleotide system; medical diagnosis;

KW functional genomics; sample analysis; pharmacogenomics; sample analysis.

XX Unidentified.

XX DE10209071-A1.

XX 25-SEP-2003.

XX 28-FEB-2002; 2002DE-01009071.

XX 28-FEB-2002; 2002DE-01009071.

XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.

XX Koehler T, Rost A;

XX WPI; 2003-732912/70.

XX Standardized polynucleotide system, useful for quantitative, real-time  
 PT determination of nucleic acid, comprises stabilized standards, primers  
 PT and probe.

XX Claim 1; Page 7; 38pp; German.

XX The present invention relates to a standardized polynucleotide system,  
 CC which comprises at least one carrier nucleic acid, at least 3  
 CC oligonucleotides, as primers and target-specific, fluorescently labeled  
 CC probe and optionally at least one set of stabilized controls (standard  
 CC RNA or DNA) of known concentration and instructions. The system comprises  
 CC any of 20 sets of one control, two primers and one target-specific probe.  
 CC The standardized polynucleotide system can be used for quantitative, real  
 CC -time detection of target nucleic acids, especially analysis of genes or  
 CC gene products, e.g. for individualized medical diagnosis, in veterinary  
 CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,

CC Pharmaceutical testing, analysis of food or environmental samples and  
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present  
CC sequence is a polynucleotide used in the system of the invention.

SQ Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 337;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACACAAAAGTATCC 18

Db 178 AGTTCACACAAAAGTATCC 161

RESULT 4

ACH46093/C

ID ACH46093 standard; cDNA; 492 BP.

AC ACH46093;

XX 13-OCT-2003 (first entry)

XX Human infant brain cDNA #156.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA//) DRMANAC R T.

XX (LABA//) LABAT I.

XX (STAC//) STACHE-CRAIN B.

XX (DICK//) DICKSON M C.

XX (JONE//) JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

DR WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful

PT as hybridization probes, as oligomers for PCR, for chromosome and gene

PT mapping, in the recombinant production of protein, or in generating

PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 33305; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of

XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was

XX determined by the technique of SBH (sequencing by hybridisation). Also

XX included is a purified polypeptide comprising a sequence corresponding to

XX a reading frame of the novel polynucleotide. The nucleic acid sequences

XX are useful in diagnostics as expressed sequence tags (EST) for

XX identifying expressed genes or for physical mapping of the human genome,

XX in forensics, in assessing biodiversity, or in identifying mutations

XX responsible for genetic disorders and other traits. The nucleotide

XX sequences are also useful as hybridisation probes, as oligomers for PCR,

XX for chromosome and gene mapping, in the recombinant production of

XX protein, or in generating antisense DNA or RNA. The purified polypeptide

XX is useful for generating antibodies specific for it. The present sequence

XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data

XX for this patent did not form part of the printed specification, but was

XX obtained in electronic format directly from USPTO at

XX seqdata.uspto.gov/sequence.html?DocID=20030073623

XX

SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 9; Length 492;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACACAAAAGTATCC 18

Db 362 AGTTCACACAAAAGTATCC 345

RESULT 5

ABA59891

ID ABA59891 standard; DNA; 587 BP.

XX

AC ABA59891;

XX

DT 01-FEB-2002 (first entry)

XX

XX Human foetal liver single exon nucleic acid probe #8196.

XX

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS

XX Homo sapiens.

XX

PN WO200157277-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000669.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GE-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-483447/52.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human foetal liver.

XX

PS Claim 1; SEQ ID NO 8196; 639pp + Sequence Listing; English.

XX

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACACAAAAGTATCC 18

Db 510 AGTTCACACAAAAGTATCC 527

RESULT 6

AAI39762

ID AAI39762 standard; DNA; 587 BP.

```

XX AC AAI39762;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #8448 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 1; SEQ ID NO 6802; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
DB 510 AGTTCACACAAAAGTATCC 527

RESULT 7
ABA28336
ID ABA28336 standard; DNA; 587 BP.
XX AC ABA28336;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #6802 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.

Query Match 100.0%; Score 18; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAAGTATCC 18
DB 510 AGTTCACACAAAAGTATCC 527

RESULT 8
AAK34040
ID AAK34040 standard; DNA; 587 BP.
XX AC AAK34040;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 8597.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

```



CC brain. They can be used to measure gene expression in brain cell samples.  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention  
XX  
XX  
SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 587;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
  
QY 1 AGTTCACACAAAGTATCC 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 510 AGTTCACACAAAGTATCC 527  
  
RESULT 10  
ABS33839  
ID ABS33839 standard; DNA; 587 BP.  
XX AC AC  
XX ABS33839;  
XX  
XX  
DT 25-FEB-2003 (first entry)  
XX  
XX Human liver single exon probe, SEQ ID NO 8829.  
DE  
XX  
XX Human; single exon nucleic acid probe; liver; cirrhosis;  
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; SB.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WC200157273-A2.  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US0000664.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488898/53.  
DR  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
XX Claim 1; SEQ ID NO 8829; 658pp; English.  
XX  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 4; Length 587;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGTTCACACAAAAGTATCC 18  
 DB 510 AGTTCACACAAAAGTATCC 527

RESULT 11  
 ABS08825  
 ID ABS08825 standard; DNA; 587 BP.  
 AC ABS08825;  
 DT 19-AUG-2002 (first entry)  
 DE Human genome-derived single exon probe from lung SEQ ID NO 8816.  
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW Chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2002-114183/15.  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX Claim 1; SEQ ID NO 8816; 634pp; English.

The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridise at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 587;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGTTCACACAAAAGTATCC 18  
 DB 510 AGTTCACACAAAAGTATCC 527

RESULT 12  
 ACH70569/c  
 ID ACH70569 standard; DNA; 587 BP.  
 XX ACH70569;  
 AC ACH70569;  
 DT 29-JUL-2004 (first entry)  
 XX Human genome derived single exon probe #3764.  
 DE Human; probe; ss; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX US2003194704-A1.  
 PN 16-OCT-2003.  
 PD 03-APR-2002; 2002US-00029386.  
 PF 03-APR-2002; 2002US-00029386.  
 PR 03-APR-2002; 2002US-00029386.  
 XX (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX Penn SG, Rank DR, Hanzel DK;  
 PI WPI; 2004-119264/12.  
 XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX Claim 15; SEQ ID NO 3764; 80pp; English.

CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subsequence, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above). The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX SQ Sequence 587 BP; 130 A; 193 C; 129 G; 135 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 587;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAGTATCC 18  
 |||||  
 Db 78 AGTTCCACAAAGTATCC 61

RESULT 13  
 AAH48169/c  
 ID AAH48169 standard; DNA; 636 BP.

XX AC AAH48169;

XX DT 21-SEP-2001 (first entry)

XX DE Mutant bcl-XL coding sequence.

XX KW BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2;  
 KW antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis;  
 KW ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases;  
 KW infective multiple failure; fulminant hepatitis; diabetes; mutant;  
 KW Bcl-XL; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200148014-A1.

XX PD 05-JUL-2001.

XX FF 26-DEC-2000; 2000WO-JP009274.

XX PR 27-DEC-1999; 99JP-00371449.

XX PA (SHIO) SHIONOGI & CO LTD.

XX PI Shimizu S, Tsujimoto Y;

XX DR WPI; 2001-418246/44.

XX DR P-PSDB; AAG64285.

XX BH4-fused polypeptides with peptide sequences capable of exerting effect  
 PT on enabling uptake into cells, applicable as effective apoptosis  
 PT inhibitors, useful in preventives or remedies for ischemic diseases e.g.  
 PT myocardial infarct.

XX PS Disclosure; Page 66-68; 84pp; Japanese.

XX The present invention relates to BH4-fused polypeptides. The BH4-fused  
 CC polypeptide have a sequence capable of affecting cellular uptake and also  
 CC a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The  
 CC BH4-fused polypeptides are useful as effective apoptosis inhibitors, and  
 CC are useful in preventives or remedies for ischaemic diseases e.g.  
 CC myocardial infarct, AIDS, neurodegenerative diseases, infective multiple  
 CC failure, fulminant hepatitis and diabetes. The present sequence is a  
 CC mutant bcl-XL sequence which was used in the present invention. This  
 CC sequence was derived from a human bcl-XL DNA sequence

XX SQ Sequence 636 BP; 148 A; 158 C; 207 G; 123 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCCACAAAGTATCC 18  
 |||||  
 Db 518 AGTTCCACAAAGTATCC 501

RESULT 14

AAH43464/c

ID AAH43464 standard; cDNA; 702 BP.

XX AC AAH43464;

XX DT 04-DEC-2001 (first entry)

XX DE cDNA clone HP03564 ORF.

XX KW NPw38; NPwBP; protein interaction; reporter function; eukaryotic cell;  
 KW localization; protein network; intracellular; primer; amplify; PCR;  
 KW polymerase chain reaction; mitochondria; ss.

XX OS Homo sapiens.

XX FN WO200168885-A1.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-JP001973.

XX PR 15-MAR-2000; 2000JP-00073095.

XX PR 24-AUG-2000; 2000JP-00254418.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Kato S, Eguchi C, Nagata N, Otake M;

XX DR WPI; 2001-590069/66.

XX DR P-PSDB; AAB47515.

XX PT Detection of protein-protein interactions for screening compounds capable  
 PT of modifying the interaction comprises observing intracellular  
 PT localization of one protein after altering the modification pattern.

XX PS Example 6; Page 27-29; 33pp; Japanese.

XX This sequence represents the open reading frame of the mitochondrial cDNA  
CC clone HP03564. The protein encoded by this sequence was used in the  
CC method of the invention. The method allows detection of interactions  
CC between a protein X and a protein Y which has a reporter function in  
CC eukaryotic cells, and comprises modifying the localization patterns of X  
CC and/or Y, and the localization of Y in the cell is observed using the  
CC reporter function. This method is useful for the elucidation of protein  
CC networks within the cell. It is also applicable for the discovery of new  
CC proteins and low-molecular drugs, by observing their effect on  
CC intracellular protein interactions  
XX  
SQ Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 5; Length 702;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTTCACACAAAAGTATCC 18  
Db 581 AGTTCACACAAAAGTATCC 564  
RESULT 15  
ADM45994/c  
ID ADM45994 standard; cDNA; 702 BP.  
XX  
AC ADM45994;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human apoptosis inhibitory factor Bcl-xL cDNA.  
XX  
KW random oligonucleotide library; protein interaction; ligand;  
KW receptor binding site; ss; gene; human; apoptosis inhibitory factor;  
KW Bcl-xL.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..702  
FT /\*tag= a  
FT /product= "Human apoptosis inhibitory factor Bcl-xL  
FT protein"  
XX  
PN JP2004024078-A.  
XX  
PD 29-JAN-2004.  
XX  
PF 24-JUN-2002; 2002JP-00183456.  
XX  
PR 24-JUN-2002; 2002JP-00183456.  
XX  
PA (SERE-) SERESUTA REKISHIKO SCI KK.  
XX  
WPI; 2004-161478/16.  
DR P-PSDB; ADM45995.  
XX  
PT Random oligonucleotide useful for detecting protein interaction, having  
PT base sequence, where each base of 1st and 2nd of the codon is the any of  
PT G, C, T (U), or A and the base of 3rd of codon is G or C, or G or T (U).  
XX  
PS Example 2; SEQ ID NO 3; 43pp; Japanese.  
XX  
CC The invention relates to a novel random oligonucleotide having a base  
CC sequence where each base of the 1st and 2nd codon is any of G, C, T (U)  
CC or A and each base of the 3rd codon is G or C, or G or T (U). The methods  
CC of the invention may be useful for preparing a random oligonucleotide  
CC preparation to be used for detecting protein interactions or for  
CC screening ligand or receptor protein binding sites. The current sequence  
CC is that of the human apoptosis inhibitory factor Bcl-xL cDNA of the  
CC invention.  
XX

SQ Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 12; Length 702;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTTCACACAAAAGTATCC 18  
Db 581 AGTTCACACAAAAGTATCC 564  
Search completed: February 4, 2005, 21:52:43  
Job time : 232.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-11  
Perfect score: 18  
Sequence: 1 agttcacacaaagtatcc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	167	2	BF929309 IL2-NT020
2	18	100.0	216	2	BF806802 PM2-C1011
3	18	100.0	231	4	BM818607 K-EST0085
4	18	100.0	232	2	BF804861 PM2-C1011
5	18	100.0	256	4	BM049697 603624202
6	18	100.0	283	2	BF823588 RCS-RT005
7	18	100.0	332	2	AW820481 QV2-ST029
8	18	100.0	358	2	AW820530 QV2-ST029
9	18	100.0	396	4	BM818649 K-EST0085
10	18	100.0	418	4	BI051278 CM3-GN029
11	18	100.0	418	4	BM741875 K-EST0014
12	18	100.0	442	1	AA903741 ok64a12.8
13	18	100.0	447	4	BM818387 K-EST0085
14	18	100.0	482	2	BM378810 601237325
15	18	100.0	486	2	AW814883 MRI-ST020
16	18	100.0	516	7	HO9884 YMO5007.r1
17	18	100.0	522	2	BE395937 601312716
18	18	100.0	555	2	BE393580 601310279
19	18	100.0	563	2	BE617040 601441454
20	18	100.0	579	4	BM741157 K-EST0013
21	18	100.0	607	5	BG636684 hdl3a09.y
22	18	100.0	620	4	BM820164 K-EST0088
23	18	100.0	652	4	BM043798 603620649
24	18	100.0	657	2	BE207063 ba09f05.y

c	25	18	100.0	681	6	CF147016 UI-HF-CB0
c	26	18	100.0	687	2	BE293685 601186941
c	27	18	100.0	695	4	BI252492 602952957
c	28	18	100.0	697	4	BI457116 603185360
c	29	18	100.0	699	2	BE870269 601447403
c	30	18	100.0	705	4	BE290422 602389270
c	31	18	100.0	714	4	BG470667 602511594
c	32	18	100.0	720	6	CD636470 56049223J
c	33	18	100.0	725	6	CD636468 56049107J
c	34	18	100.0	737	4	BG748447 602706419
c	35	18	100.0	765	2	BF569393 602185659
c	36	18	100.0	767	2	BE512918 601172142
c	37	18	100.0	782	2	BE249973 600943141
c	38	18	100.0	798	5	BQ687097 AGENCOURT
c	39	18	100.0	798	5	BUS28551 AGENCOURT
c	40	18	100.0	798	7	CK000319 AGENCOURT
c	41	18	100.0	808	4	BI222971 602943462
c	42	18	100.0	817	5	BQ943707 AGENCOURT
c	43	18	100.0	830	7	CF619432 AGENCOURT
c	44	18	100.0	843	5	BQ921211 AGENCOURT
c	45	18	100.0	843	5	BQ962018 AGENCOURT

ALIGNMENTS

RESULT 1  
BF929309  
LOCUS 167 bp mRNA linear EST 19-JAN-2001  
DEFINITION IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF929309  
VERSION BF929309.1 GI:12327437  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 167)  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correea,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 167.  
Location/Qualifiers  
1. .167  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NT0202"  
/notes="Organ: nervous tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

QY 1 AGTTCACAAAAGTATCC 18  
|||||  
Db 147 AGTTCACAAAAGTATCC 164

## RESULT 2

BF806802  
LOCUS PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
ACCESSION BF806802  
VERSION BF806802.1 GI:12135791  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 216)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, U.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PubMed 10737800

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-091100-004-b10&t3=2000-11-09&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 25  
High quality sequence stop: 216.

## FEATURES

source

1..216  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CI0111"  
/note="Organ: colon ins; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
Derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18  
|||||  
Db 146 AGTTCACAAAAGTATCC 163

## RESULT 3

BF818607  
LOCUS PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
ACCESSION BF818607  
VERSION BF818607.1 GI:19175020  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 231)  
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 4 Row: B Column: 02  
High quality sequence stop: 231.

Location/Qualifiers  
1..231  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S20T665307-4-B02"  
/sex="M"  
/lab\_host="Top10F"  
/clone\_lib="S20T665307"  
/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI;  
Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tabacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dT-selected mRNA by  
priming with dT-tailed vector. The dT-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F, by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

Query Match 100.0%; Score 18; DB 4; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

QY 1 AGTTCACAAAAGTATCC 18  
|||||  
Db 215 AGTTCACAAAAGTATCC 198

## RESULT 4

BF804861  
LOCUS PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
ACCESSION BF804861

```

VERSION      BF804861.1  GI:12133850
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 232)
AUTHORS      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-
              041100-001-401&t3=2000-11-04&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 13
              High quality sequence stop: 232.
              Location/Qualifiers
FEATURES     source
              1..232
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="CI0111"
                /note="Organ: colon ins; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAGTATCC 18
    |||||
Db 162 AGTTCACACAAAGTATCC 179

RESULT 5
BM049697/c
LOCUS          BM049697      256 bp      mRNA      linear      EST 07-NOV-2001
DEFINITION    603624202F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5450041 5',
              mRNA sequence.
ACCESSION     BM049697
VERSION       BM049697.1  GI:16778964
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 256)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              TITLE

```

```

JOURNAL      Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DTF
              CDNA Library Preparation: Ling Hong/Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1938 row: c column: 02
              High quality sequence stop: 171.
              Location/Qualifiers
FEATURES     source
              1..256
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5450041"
                /tissue_type="carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_40"
                /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
                Site 2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCAGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-CDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACACAAAGTATCC 18
    |||||
Db 64 AGTTCACACAAAGTATCC 47

RESULT 6
BF823588
LOCUS          BF823588      283 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION    RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF823588
VERSION       BF823588.1  GI:12164528
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 283)
AUTHORS       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL

```

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-221200-011-G02&t3=2000-12-22&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 283.

## FEATURES

source  
 1. .283  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="RT0055"

/note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18  
 |||||  
 Db 192 AGTTCACAAAAGTATCC 209

## RESULT 7

AW820481/c  
 LOCUS 332 bp mRNA linear EST 17-MAY-2000  
 DEFINITION QV2-ST0298-142000-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW820481  
 VERSION AW820481.1 GI:7913475  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 332)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=QV2-ST0298-140200-042-f12&t3=2000-02-14&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 332.

Location/Qualifiers

1. .332

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCACAAAAGTATCC 18  
 |||||  
 Db 182 AGTTCACAAAAGTATCC 165

## RESULT 8

AW820530/c  
 LOCUS 358 bp mRNA linear EST 17-MAY-2000  
 DEFINITION QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW820530  
 VERSION AW820530.1 GI:7913524  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 358)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=QV2-ST0298-220200-061-d10&t3=2000-02-22&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 44

High quality sequence stop: 358.

Location/Qualifiers

1. .358

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="ST0298"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 358;



```

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18
Db 196 AGTTCACAAAAGTATCC 179

RESULT 9
BM818649/c
LOCUS
DEFINITION K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
5', mRNA sequence.
ACCESSION BM818649
VERSION BM818649.1 GI:19175062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 03
High quality sequence stop: 396.
FEATURES
source
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-4-F03"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pcMS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18
Db 215 AGTTCACAAAAGTATCC 198

RESULT 10
BI051278
LOCUS
DEFINITION CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI051278
VERSION BI051278.1 GI:14458808
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 418)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,C.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-
110101-607-f03&t3=2001-01-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 418.
FEATURES
source
1..418
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_stage="Adult"
/clone_lib="GN0297"
/note="Organ: placenta normal; Vector: puc18; Site 1:
SmaI; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18
Db 144 AGTTCACAAAAGTATCC 161

RESULT 11
BM741875/c
LOCUS
DEFINITION K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-Col 5',
mRNA sequence.
ACCESSION BM741875
VERSION BM741875.1 GI:19063204
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS 1 (bases 1 to 418)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,O.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 Row: C Column: 01
High quality sequence stop: 418.
Location/Qualifiers
FEATURES
source 1..418
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620-4-C01"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10P"
/clone_lib="S6SNU620"
/notes="Organ: Stomach; Vector: pCNS; Site:1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Query Match 100.0%; Score 18; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTTCACAAAAGTATCC 18
|||||
Db 87 AGTTCACAAAAGTATCC 70
RESULT 12
AA903741 442 bp mRNA linear EST 09-JUN-1998
LOCUS Ok64a12.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518718 3'
DEFINITION similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. i, mRNA
sequence.
ACCESSION AA903741.1 GI:3038864
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the i.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 536 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
FEATURES
source 1..442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518718"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/notes="Vector: pYT3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia) digested with Not I and cloned
into the Not I and Eco RI sites of the modified pYT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTTCACAAAAGTATCC 18
|||||
Db 388 AGTTCACAAAAGTATCC 405
RESULT 13
BM818387/c 447 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
DEFINITION 5', mRNA sequence.
ACCESSION BM818387
VERSION BM818387.1 GI:19174800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 3 Row: B Column: 02
High quality sequence stop: 447.
Location/Qualifiers
FEATURES
source 1..447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-3-B02"
/sex="M"

```

/lab\_host="Top10F"  
 /clone\_lib="S20T65307"  
 /note="Organ: Stomach; Vector: pcns; Site 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18  
 |||||  
 Db 215 AGTTCACAAAAGTATCC 198

## RESULT 14

BE378810/c  
 LOCUS BE378810 482 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601237325F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3609126 5',  
 mRNA sequence.

ACCESSION BE378810 GI:9324175

VERSION BE378810.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 482)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM263 row: b column: 07

High quality sequence start: 4

High quality sequence stop: 479.

## FEATURES

source

1..482  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="NIH\_MGC\_44"  
 /tissue\_type="endometrium, adenocarcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_44"  
 /note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 482;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18  
 |||||  
 Db 153 AGTTCACAAAAGTATCC 136

## RESULT 15

AW814883

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

1 (bases 1 to 486)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MRI-ST0206-120

400-022-f04&t3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 55

High quality sequence stop: 485.

Location/Qualifiers

1..486

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="ST0206"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 486;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTTCACAAAAGTATCC 18  
 |||||  
 Db 106 AGTTCACAAAAGTATCC 123

Search completed: February 5, 2005, 08:11:52  
Job time : 2147.2 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-12  
Perfect score: 18  
Sequence: 1 ctttcggctctcgctgc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235160
2	18	100.0	18	6	BD235180
3	18	100.0	18	6	BD235181
4	18	100.0	127	6	CQ112670
5	18	100.0	127	6	CQ151543
6	18	100.0	127	6	CQ185285
7	18	100.0	127	6	CQ234920
8	18	100.0	127	6	CQ272476
9	18	100.0	127	6	CQ310145
10	18	100.0	127	6	CQ346752
11	18	100.0	387	6	CQ732731
12	18	100.0	587	6	CQ099589
13	18	100.0	587	6	CQ138575
14	18	100.0	587	6	CQ175406
15	18	100.0	587	6	CQ221990
16	18	100.0	587	6	CQ259335
17	18	100.0	587	6	CQ297711
18	18	100.0	587	6	CQ334058
19	18	100.0	636	6	BD097037

c 20	18	100.0	702	6	BD084108
c 21	18	100.0	702	6	BD102202
c 22	18	100.0	702	9	BT007208
c 23	18	100.0	702	12	BT008248
c 24	18	100.0	737	6	AR054022
c 25	18	100.0	737	6	AR172595
c 26	18	100.0	737	6	IS2012
c 27	18	100.0	737	6	AR371662
c 28	18	100.0	737	6	AR380913
c 29	18	100.0	737	9	HSBCLXS
c 30	18	100.0	747	6	AX127722
c 31	18	100.0	926	6	AR054021
c 32	18	100.0	926	6	AR118504
c 33	18	100.0	926	6	AR124952
c 34	18	100.0	926	6	AR144311
c 35	18	100.0	926	6	AR172594
c 36	18	100.0	926	6	BD243042
c 37	18	100.0	926	6	CQ765842
c 38	18	100.0	926	6	E58777
c 39	18	100.0	926	6	IS2011
c 40	18	100.0	926	6	AR371661
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

ALIGNMENTS

RESULT 1  
LOCUS BD235160 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
ACCESSION BD235160  
VERSION BD235160.1 GI:33044930  
KEYWORDS JP 2002519048-A/12.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein,C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 12 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/12  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC  
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence',  
Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630',

FEATURES

source  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630',

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CTTTCGGCTCTCGCTGC 18  
|||||||

```

Db          1 CTTTCGGCTCTCGGCTGC 18
RESULT 2
BD235180
LOCUS      BD235180
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235180
VERSION    BD235180.1 GI:33044950
KEYWORDS  JP 2002519048-A/32.
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 32 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/32
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
PH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT misc_binding (8)..(9)
FT misc_binding (10)..(12)
FT misc_binding (15)..(18)
FT misc_binding (16)..(16)
FT modified_base (2)..(4)
FT modified_base (8)..(8)
FT modified_base (9)..(9)
FT modified_base (10)..(10)
FT modified_base (11)..(11)
FT modified_base (12)..(12)
FT modified_base (15)..(15)
FT modified_base (16)..(16)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 1 CTTTCGGCTCTCGGCTGC 18
|||||
RESULT 4
CQ112670
LOCUS      CQ112670
DEFINITION Sequence 21529 from Patent WO0157272.
ACCESSION  CQ112670
VERSION    CQ112670.1 GI:41082540
KEYWORDS   Location/Qualifiers
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
           Patent: WO 0157272-A 21529 09-AUG-2001;
           Aeomica, Inc. (US)
JOURNAL
FEATURES
source
1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
Db          1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 1 CTTTCGGCTCTCGGCTGC 18
|||||
RESULT 3
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 1 CTTTCGGCTCTCGGCTGC 18
|||||

```

```

BD235181
LOCUS      BD235181
DEFINITION Oligonucleotide inhibitors of bcl-xL.
ACCESSION  BD235181
VERSION    BD235181.1 GI:33044951
KEYWORDS  JP 2002519048-A/33.
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 33 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT    OS Artificial Sequence
           PN JP 2002519048-A/33
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC
C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
PH Key Location/Qualifiers
FT misc_binding (1)..(4)
FT misc_binding (8)..(9)
FT misc_binding (10)..(12)
FT misc_binding (15)..(18)
FT misc_binding (16)..(16)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTCGGCTCTCGGCTGC 18
|||||
Db 1 CTTTCGGCTCTCGGCTGC 18
|||||
RESULT 4
CQ112670
LOCUS      CQ112670
DEFINITION Sequence 21529 from Patent WO0157272.
ACCESSION  CQ112670
VERSION    CQ112670.1 GI:41082540
KEYWORDS   Location/Qualifiers
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE      Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
           Patent: WO 0157272-A 21529 09-AUG-2001;
           Aeomica, Inc. (US)
JOURNAL
FEATURES
source
1..127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =

```

1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:  
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 5

CQ151543  
LOCUS CQ151543 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21565 from Patent WO0157276.  
ACCESSION CQ151543  
VERSION CQ151543.1 GI:41158893  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 21565 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL  
= 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN  
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 6

CQ185285  
LOCUS CQ185285 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 16681 from Patent WO0157274.  
ACCESSION CQ185285  
VERSION CQ185285.1 GI:41180300  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human heart  
JOURNAL Patent: WO 0157274-A 16681 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL =  
1.6-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:  
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 7

CQ234920  
LOCUS CQ234920 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21759 from Patent WO0157273.  
ACCESSION CQ234920  
VERSION CQ234920.1 GI:41218197  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
(03.10.00)<150> US 60/236,359<151> 27 September 2000  
(27.09.00)<150> US 60/234,687<151> 21 September 2000  
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
Patent: WO 0157273-A 21759 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL  
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN  
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

## JOURNAL

Patent: WO 0157273-A 21759 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source  
1..127  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL  
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN  
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE  
1.00e-65"

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 8

CQ272476  
LOCUS CQ272476 127 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 20737 from Patent WO0157277.  
ACCESSION CQ272476  
VERSION CQ272476.1 GI:41245080  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for





```
JOURNAL Patent: WO 0157272-A 8448 09-AUG-2001;
FEATURES   Aecomica, Inc. (US)
source     1. .587
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
           1.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

RESULT 13
CQ138575
LOCUS      CQ138575          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 8597 from Patent WO0157276.
ACCESSION  CQ138575
VERSION    CQ138575.1 GI:41095941
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
           ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
           3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
           60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
           August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
           (03.10.00)<150> US 60/236,359<151> 27 September 2000
           (27.09.00)<150> US 60/234,687<151> 21 September 2000
           (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
           Molecular Dynamics Sequence Listing Engine
           Patent: WO 0157273-A 8829 09-AUG-2001;
           Aecomica, Inc. (US)
JOURNAL    Location/Qualifiers
FEATURES   source
           1. .587
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
           = 5.5"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

RESULT 14
CQ175406
LOCUS      CQ175406          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 6802 from Patent WO0157274.
ACCESSION  CQ175406
VERSION    CQ175406.1 GI:41170145
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE      HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
           ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
           PATENT: WO 0157274-A 6802 09-AUG-2001;
           Aecomica, Inc. (US)
JOURNAL    Location/Qualifiers
FEATURES   source
           1. .587
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           /note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
           = 1.9"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 476 CTTTCGGCTCTCGGCTGC 493

Search completed: February 4, 2005, 23:30:42
Job time : 432.664 secs
```

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-12  
Perfect score: 18  
Sequence: 1 ctttcggtctcgctgc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	Az46982 Bcl-Xl mR
2	18	100.0	25	12	ADP17303 Renal cel
3	18	100.0	70	10	ADG89109
4	18	100.0	70	12	ADP27571 Human Bcl
5	18	100.0	127	4	ABA72432 Human foe
6	18	100.0	127	4	ABA72432 Human foe
7	18	100.0	127	4	ABA38215 Probe #21
8	18	100.0	127	4	ABA38215 Probe #16
9	18	100.0	127	4	AAK47008 Human bon
10	18	100.0	127	4	AAK20855 Human bra
11	18	100.0	127	6	ABS46769 Human liv
12	18	100.0	127	6	ABS21259 Human gen
13	18	100.0	179	12	ACH84269 Human gen
14	18	100.0	299	10	ACD94503 Human col
15	18	100.0	337	10	ADK66037 Standard
16	18	100.0	492	9	ACH46093 Human inf
17	18	100.0	587	4	ABA59891 Human foe
18	18	100.0	587	4	AAI39762 Probe #84
19	18	100.0	587	4	ABA28336 Probe #68
20	18	100.0	587	4	AAK34040 Human bon
21	18	100.0	587	4	AAK08161 Human bra
22	18	100.0	587	4	ABS33839 Human liv

22	18	100.0	587	6	ABS08825	Abs08825 Human gen
23	18	100.0	587	12	ACH70569	Ach70569 Human gen
24	18	100.0	636	4	AAH48169	Aah48169 Mutant bc
25	18	100.0	702	5	AAH43464	Aah43464 cDNA clon
26	18	100.0	702	12	ADM45994	Adm45994 Human apo
27	18	100.0	737	2	AAQ81698	Aaq81698 Human thy
28	18	100.0	737	10	ABZ83507	Abz83507 Toxicolog
29	18	100.0	737	11	ADI32132	Adi32132 Human cDN
30	18	100.0	739	12	ADG65218	Adg65218 Human Bcl
31	18	100.0	747	4	AAF30926	Aaf30926 Human Bcl
32	18	100.0	747	12	ADG65209	Adg65209 Human Bcl
33	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
34	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
35	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-X gen
36	18	100.0	926	4	AAAS15189	Aas15189 Human bcl
37	18	100.0	926	4	AAC90810	Aac90810 Human Bcl
38	18	100.0	926	6	ABK84766	Abk84766 Human cDN
39	18	100.0	926	8	ABT16641	Abt16641 Human bcl
40	18	100.0	926	10	ADD56779	Add56779 Human bcl
41	18	100.0	926	10	ADD64187	Add64187 Human bcl
42	18	100.0	926	11	ADI32104	Adi32104 Human cDN
43	18	100.0	926	12	ADH52630	Adh52630 Human ant
44	18	100.0	926	12	ADO19990	Ado19990 Human PRO
45	18	100.0	926	12	ADP13351	Adp13351 Renal cel

## ALIGNMENTS

## RESULT 1

AZ46982  
ID AAZ46982 standard; DNA; 18 BP.

AC AAZ46982;

DT 14-APR-2000 (first entry)

XX Bcl-Xl mRNA specific antisense oligo L.

XX Anti-apoptotic protein; bcl-XL; tumour; cancer; epithelial; prostate;  
XX lung; bladder; bcl-2; vascular lesion; antisense; ss.

OS Homo sapiens.

XX WO200001393-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US015250.

XX 02-JUL-1998; 98US-00109614.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Stein CA;

XX WPI; 2000-137140/12.

XX New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-XL, useful for reducing bcl-XL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

XX Claim 1; Fig 1; 69pp; English.

XX The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-XL. The oligonucleotides can be introduced into tumour cells to reduce bcl-XL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-XL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-XL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
CC represent antisense oligos specific for the bcl-X1 mRNA

XX Sequence 18 BP; 0 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 1 CTTTCGGCTCTCGGCTGC 18

RESULT 2  
ADP17303/c  
ID ADP17303 standard; DNA; 25 BP.  
XX AC ADP17303;  
XX DT 26-AUG-2004 (first entry)  
XX DE Renal cell carcinoma differentially expressed gene probe #3708.  
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression; probe.  
XX OS Homo sapiens.

XX WO2004048933-A2.  
XX 10-JUN-2004.  
XX 21-NOV-2003; 2003WO-US037481.  
XX 21-NOV-2002; 2002US-0427982P.  
PR 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;

XX WPI; 2004-460799/43.  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.  
XX Disclosure; SEQ ID NO 4039; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.

SQ Sequence 25 BP; 8 A; 6 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 23 CTTTCGGCTCTCGGCTGC 6

RESULT 3  
ADG89109/c  
ID ADG89109 standard; DNA; 70 BP.  
XX AC ADG89109;  
XX DT 11-MAR-2004 (first entry)  
XX DE Cancer detection method related oligonucleotide #57.  
XX ss; cancer; gene expression;  
KW estrogen receptor-positive invasive breast cancer.

XX OS Homo sapiens.  
XX WO2003078662-A1.  
XX 25-SEP-2003.  
XX 12-MAR-2003; 2003WO-US007713.  
XX 13-MAR-2002; 2002US-0364890P.  
PR 18-SEP-2002; 2002US-0412049P.

XX (GENO-) GENOMIC HEALTH INC.  
XX Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;  
XX WPI; 2003-767536/72.  
XX Predicting clinical outcome for a patient diagnosed with cancer comprises  
PT determining the expression level of one or more genes, and compared to  
PT the amount found in a reference cancer tissue set.

XX Disclosure; SEQ ID NO 57; 198pp; English.

XX The invention relates to a method of predicting clinical outcome for a  
CC patient diagnosed with cancer by determining the expression level of one  
CC or more genes, or their expression products, selected from p53BP2,  
CC cathepsin B, cathepsin L, ki67/MiB1, and thymidine kinase in a cancer  
CC tissue obtained from the patient, normalized against control gene(s), and  
CC compared to the amount found in a reference cancer tissue set. The  
CC specification also discloses an array comprising polynucleotides  
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-  
CC 67, GSTM1, CA9, PR, BRC3, NME1, SURV, GATA3, TERC, YB-1, DPYD, GSTM3,  
CC RPS8KB1, Sro, Chkl, ID1, EstR1, p27, CCNE1, XIAP, Chk2, CDC25B, IGFBP3,  
CC AK055699, P13KC2A, TGFB3, BAG1, CYP3A4, EPCAM, VEGFC, PS2, HENT1, WISP1,  
CC HNF1A, NFKBp65, BRC3, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFIA,  
CC CDH1, HIF1, IGFBP3, CTSS, Her2 and DIABLO, immobilized on a solid  
CC surface. The methods are useful for predicting clinical outcome for a  
CC patient diagnosed with cancer, classifying cancer, and predicting the  
CC likelihood of long-term survival of a breast cancer patient, or a patient  
CC diagnosed with invasive breast cancer or with estrogen receptor (ER) -  
CC positive invasive breast cancer. This sequence corresponds to an  
CC oligonucleotide used in the method of the invention.

XX Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 70;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGGCTCTCGGCTGC 18  
DB 47 CTTTCGGCTCTCGGCTGC 30

## RESULT 4

ID ADP27571/c

ADP27571 standard; DNA; 70 BP.

XX AC

XX ADP27571;

XX DT 26-AUG-2004 (first entry)

XX DE

XX Human Bclx DNA used as a cancer prognostic marker SeqID 8.

XX KW

XX Bclx; human; PCR amplicon; ds; prognostic marker; EGFR;

XX KW epidermal growth factor receptor; cancer; gene expression profiling;

XX KW microarray; head and neck cancer; colon cancer; metastatic spread;

XX KW neoplastic disease.

XX OS

XX Homo sapiens.

XX FN

XX WO2004046386-A1.

XX PD

XX 03-JUN-2004.

XX PF

XX 14-NOV-2003; 2003WO-US036777.

XX PR

XX 15-NOV-2002; 2002US-0427090P.

XX PA

XX (GENO-) GENOMIC HEALTH INC.

XX PA (VALL-) VALL HEBRON UNIV HOSPITAL.

XX PI

XX Baker JB, Cronin MT, Shak S, Baselga J;

XX DR

XX WPI; 2004-420643/39.

XX PT

XX Prognosing a patient with EGFR-expressing colon cancer comprises

XX PT subjecting a sample comprising EGFR-expressing cancer cells to

XX PT quantitative analysis of the expression level of the RNA transcript of at

XX PT least one gene e.g., CD44v3.

XX PS

XX Claim 55; SEQ ID NO 8; 113pp; English.

XX CC

XX This invention relates to a novel method concerning prognostic markers

XX CC associated with EGFR (epidermal growth factor receptor) positive cancer.

XX CC Specifically, it refers to a gene expression profiling method that can

XX CC provide a prediction as to whether a patient is likely to respond well to

XX CC treatment with an EGFR inhibitor. The present invention describes the

XX CC quantitative analysis of the expression level of the RNA transcript of at

XX CC least one gene selected from the group of CD44v3, CD44v6, DR5, cGRO1,

XX CC KR17, LAMC2 or their products thereof. It further provides a cDNA

XX CC microarray containing named genes that represent prognostic transcripts

XX CC which are useful for determining whether a patient diagnosed with an EGFR

XX CC -expressing head or neck cancer or colon cancer exhibits elevated or

XX CC decreased expression levels of these genes compared to normal. As such,

XX CC these methods are also useful for prognosing or predicting the likelihood

XX CC of cancer-attributable death or progression, including recurrence and

XX CC metastatic spread of a neoplastic disease, as well as drug resistance.

XX CC This polynucleotide sequence is a human PCR amplicon DNA sequence used as

XX CC a prognostic cancer marker, given in an exemplification of the invention.

XX SQ

XX Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 18; DB 12; Length 70;

XX Matches

XX 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGGCTCTCGGCTGC 18

DB 47 CTTTCGGCTCTCGGCTGC 30

## RESULT 5

ABA72432

ID ABA72432 standard; DNA; 127 BP.

XX AC

XX ABA72432;

XX DT

XX 01-FEB-2002 (first entry)

XX DE

XX Human foetal liver single exon nucleic acid probe #20737.

XX KW

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS

XX Homo sapiens.

XX FN

XX WO200157277-A2.

XX PD

XX 09-AUG-2001.

XX PF

XX 30-JAN-2001; 2001WO-US000669.

XX PR

XX 04-FEB-2000; 2000US-0180312P.

XX PR

XX 26-MAY-2000; 2000US-0207456P.

XX PR

XX 30-JUN-2000; 2000US-00608408.

XX PR

XX 03-AUG-2000; 2000US-00632366.

XX PR

XX 21-SEP-2000; 2000US-0234687P.

XX PR

XX 27-SEP-2000; 2000US-0236359P.

XX PR

XX 04-OCT-2000; 2000GB-00024263.

XX PA

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PI

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX XX

XX WPI; 2001-483447/52.

XX PT

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human foetal liver.

XX PS

XX Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.

XX CC

XX The invention relates to a single exon nucleic acid probe for measuring

XX CC human gene expression in a sample derived from human foetal liver. The

XX CC single exon nucleic acid probes may be used for predicting, measuring and

XX CC displaying gene expression in samples derived from human foetal liver. The

XX CC present sequence is a single exon nucleic acid probe of the invention.

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

OY

1 CTTTCGGCTCTCGGCTGC 18

DB

77 CTTTCGGCTCTCGGCTGC 94

## RESULT 6

AAI52843

ID AAI52843 standard; DNA; 127 BP.

XX AC

XX AAI52843;

XX DT

XX 17-OCT-2001 (first entry)

XX DE

XX Probe #21529 used to measure gene expression in human placenta sample.

XX XX

```
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 21529; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
Db |||||
77 CTTTCGGCTCTCGGCTGC 94

RESULT 7
ABA38215
ID ABA38215 standard; DNA; 127 BP.
XX
AC ABA38215;
XX
XX 23-JAN-2002 (first entry)
XX
DE Probe #16681 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.

KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 21529; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
Db |||||
77 CTTTCGGCTCTCGGCTGC 94

RESULT 8
AAK47008
ID AAK47008 standard; DNA; 127 BP.
XX
AC AAK47008;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 21565.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
```

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.

PS Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
XX the probes of the invention

SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 9

AAK20855

ID AAK20855 standard; DNA; 127 BP.

AC AAK20855;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 20846.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KW ss.

XX Homo sapiens.

OS WO200157275-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000667.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.

PS Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention

SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
Db 77 CTTTCGGCTCTCGGCTGC 94

## RESULT 10

ABS46769

ID ABS46769 standard; DNA; 127 BP.

XX AC ABS46769;

XX DT 25-FEB-2003 (first entry)

XX Human liver single exon probe, SEQ ID NO 21759.

DE Human; single exon nucleic acid probe; liver; cirrhosis;  
XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; ss.

XX Homo sapiens.

OS WO200157273-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000664.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.

XX Claim 4; SEQ ID NO 21759; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 11

ABS21259

ID ABS21259 standard; DNA; 127 BP.

XX ABS21259;

AC ABS21259;

DT 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe ORF from lung SEQ ID NO 21250.

XX Human; db; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease; open reading frame; ORF.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234887P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

XX Claim 4; SEQ ID NO 21250; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a single exon probe open reading frame of the

CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 127;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18

Db 77 CTTTCGGCTCTCGGCTGC 94

RESULT 12

ACH84269/c

ID ACH84269 standard; DNA; 179 BP.

XX ACH84269;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #17464.

XX Human; probe; ss; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

XX surveying tissues.

PS Claim 1; SEQ ID NO 17464; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-



CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above). The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterizing  
CC alternative splicing events, in detecting and characterizing gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
XX  
SQ Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 179;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
Db 71 CTTTCGGCTCTCGGCTGC 54

RESULT 13  
ACD94503/C  
ID ACD94503 standard; cDNA; 299 BP.

XX AC ACD94503;  
XX  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE Human colon cancer cell expressed cDNA #2915.

XX Open reading frame detection; genome sequencing; colon cancer;  
XX breast cancer; population genome analysis; genetic shift; cancer;  
XX antibiotic resistance; antibiotic non-tolerance; congenital disease;  
XX agriculture; food crop genome; resistance gene; retrovirus;  
XX influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;  
XX gene; ss.

XX Homo sapiens.  
XX  
XX US2002155438-A1.  
XX  
XX 24-OCT-2002.

XX 27-SEP-1999; 99US-00406117.  
XX  
XX 20-NOV-1998; 98US-00196716.

XX (SIMP// SIMPSON A J G.  
XX (NETO// NETO E D.  
XX (BREN// BRENTANI R R.

XX Simpson AJG, Neto ED, Brentani RR;

XX

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human  
suffering from cancer involves use of single oligonucleotide primer at  
low stringency for preparing single-stranded cDNA from mRNA of  
individual.

Example 9; Page 432; 959pp; English.

The invention describes a method of determining open reading frames in  
the genome of organism, comprising contacting mRNA from cell of organism  
with a single oligonucleotide primer (1) at low stringency, preparing  
single-stranded cDNA by reverse transcribing mRNA with (1), amplifying  
cDNA, sequencing the product, and repeating the contacting, preparing  
and amplifying steps with different primers and sequencing resulting  
nucleic acids. The method is useful for: determining that a known  
nucleotide sequence from a genome of an organism corresponds to a  
nucleotide sequence of an open reading frame; for preparing a contig,  
nucleic acid molecule from a genome of an organism; and for sequencing  
all or part of a genome of an organism. mRNA is obtained from mammalian  
or human cell which is associated with a pathological condition e.g. a  
colon cancer or breast cancer cell. The method is useful for analyses of  
populations of subjects and can be used to carry out genetic analyses of  
large or small populations. Further, it can be used to study living  
systems to determine if, e.g. there have been genetic shifts which render  
an individual or population more or less likely to be afflicted with  
diseases such as cancer, to determine antibiotic resistance or non-  
tolerance, and so forth. The method can also be used in the study of  
congenital diseases, and the risk of affliction to a fetus, as well as  
the study of whether the conditions are likely to be passed to offspring  
through ova or sperm. The analyses for pathological conditions can be  
carried out in all animals, plants, birds, fish, etc. Using this method,  
in the area of agriculture, for example the genomes of food crops can be  
studied to determine if resistance genes are present. Defects in plant  
genomes can also be studied in this way. Similarly, the method permits  
determination of the pathogens which integrate into the genome, such as  
retroviruses and other integrating viruses such as influenza virus, have  
undergone shifts or mutations, which may require different approaches to  
therapy. This method is also applied to eukaryotic pathogens, such as  
trypanosomes, different types of Plasmodium, etc. The method essentially  
eliminates sequencing of non-coding portions. This sequence represents a  
polynucleotide isolated from human colon cancer cell cDNA library

Sequence 299 BP; 64 A; 95 C; 74 G; 66 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 299;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
Db 49 CTTTCGGCTCTCGGCTGC 32

RESULT 14  
ADK66037/C  
ID ADK66037 standard; DNA; 337 BP.

XX AC ADK66037;

XX 06-MAY-2004 (first entry)

Standardized polynucleotide system polynucleotide #8.

ss; standardized polynucleotide system; medical diagnosis;  
functional genomics; sample analysis; pharmacogenomics; sample analysis.  
Unidentified.

DEL0209071-A1.

25-SEP-2003.

XX



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-12

Perfect score: 18  
Sequence: 1 ctttcggtctcgctgc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hc.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gsl1.\*
- 9: gb\_gsl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	167	BF929309	IL2-NT020
2	18	100.0	216	BF906802	PM2-CI011
3	18	100.0	232	BF804861	PM2-CI011
C 4	18	100.0	233	AI904167	CM-BT043-
5	18	100.0	283	BF823588	RCS-RT005
C 6	18	100.0	332	AW820481	QV2-ST029
C 7	18	100.0	339	BE925384	PMO-AN008
C 8	18	100.0	358	AW820530	QV2-ST029
C 9	18	100.0	396	AW818649	K-EST0085
10	18	100.0	418	BI051278	CM3-GN029
C 11	18	100.0	418	AW741875	K-EST0014
12	18	100.0	442	AA903741	Ok64a12.8
C 13	18	100.0	447	AW818387	K-EST0085
C 14	18	100.0	482	BE378810	601237325
C 15	18	100.0	503	AW857244	K-EST0141
C 16	18	100.0	516	H09884	Ym05007.r1
C 17	18	100.0	522	BE395937	601312716
C 18	18	100.0	555	BE393580	601310279
C 19	18	100.0	563	BE317040	601441454
C 20	18	100.0	579	BM741157	K-EST0013
C 21	18	100.0	607	BQ636684	hd3a09.y
C 22	18	100.0	620	AW820164	K-EST0088
C 23	18	100.0	652	BM043798	603620649
C 24	18	100.0	681	CF147016	UI-HF-CBO

C 25	18	100.0	687	2	BE293685	601186941
C 26	18	100.0	695	4	BE125492	602952957
C 27	18	100.0	699	2	BE870269	601447403
C 28	18	100.0	700	4	BG831301	602766132
C 29	18	100.0	705	4	BG290422	602388270
C 30	18	100.0	714	4	BG470667	603511594
C 31	18	100.0	720	6	CD636470	56049223J
C 32	18	100.0	725	6	CD636468	56049107J
C 33	18	100.0	728	4	BG169629	602321289
C 34	18	100.0	737	4	BG748447	602706419
C 35	18	100.0	739	4	BG437506	602489238
C 36	18	100.0	765	2	BF569393	602185559
C 37	18	100.0	765	2	BE873153	601451667
C 38	18	100.0	767	2	BE512918	601172142
C 39	18	100.0	782	2	BE249973	600943141
C 40	18	100.0	798	5	BQ687097	AGENCOURT
C 41	18	100.0	798	5	BU528551	AGENCOURT
C 42	18	100.0	798	7	CK000319	AGENCOURT
C 43	18	100.0	803	4	BG744242	602723349
C 44	18	100.0	808	4	BI222971	602943462
C 45	18	100.0	817	5	BQ943707	AGENCOURT

ALIGNMENTS

RESULT 1  
BF929309  
LOCUS 167 bp mRNA linear EST 19-JAN-2001  
DEFINITION IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF929309  
VERSION BF929309.1 GI:12327437  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 167)  
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2&t2=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 167.  
Location/Qualifiers  
1. 167  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NT0202"  
/notes="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 113 CTTTCGGCTCTCGGCTGC 130

## RESULT 2

BF806802  
LOCUS  
DEFINITION PM2-CI0111-091100-004-b10 CI0111 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF806802  
VERSION BF806802.1 GI:12135791  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PubMed 10737800

## COMMENT

Contact: Simpson A.J.J.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-CI0111-091100-004-b10&t3=2000-11-09&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 25  
High quality sequence stop: 216.

## FEATURES

source  
1..216  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CI0111"  
/notes="Organ: colon ins; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 112 CTTTCGGCTCTCGGCTGC 129

## RESULT 3

BF804861  
LOCUS  
DEFINITION PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF804861  
VERSION BF804861.1 GI:12133850  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PubMed 10737800

## COMMENT

Contact: Simpson A.J.J.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-CI0111-041100-001-d01&t3=2000-11-04&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 13  
High quality sequence stop: 232.

## FEATURES

source  
1..232  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CI0111"  
/notes="Organ: colon ins; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 128 CTTTCGGCTCTCGGCTGC 145

## RESULT 4

AI904167/c  
LOCUS  
DEFINITION CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AI904167

```

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
ORIGIN

```

A1904167.1 GI:6494554  
 EST.  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 233)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html  
 &t3=090299&t4=1)  
 Seq primer: puc 18 forward.  
 Location/Qualifiers  
 1..233  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /sex="female"  
 /dev\_stage="Adult"  
 /clone\_lib="BT043"  
 /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the pUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

Query Match 100.0%; Score 18; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTCGGCTCTCGGCTGC 18  
 |||||  
 Db 49 CTTTCGGCTCTCGGCTGC 32

RESULT 5  
 LOCUS  
 DEFINITION BF823588 283 bp mRNA linear EST 13-JAN-2001  
 ACCESSION BF823588  
 VERSION BF823588.1 GI:12164528  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 283)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

A1904167.1 GI:6494554  
 EST.  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 233)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html  
 &t3=090299&t4=1)  
 Seq primer: puc 18 forward.  
 Location/Qualifiers  
 1..233  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /sex="female"  
 /dev\_stage="Adult"  
 /clone\_lib="BT043"  
 /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the pUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

Query Match 100.0%; Score 18; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTCGGCTCTCGGCTGC 18  
 |||||  
 Db 49 CTTTCGGCTCTCGGCTGC 32

RESULT 5  
 LOCUS  
 DEFINITION BF823588 283 bp mRNA linear EST 13-JAN-2001  
 ACCESSION BF823588  
 VERSION BF823588.1 GI:12164528  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 283)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

```

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
ORIGIN

```

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-  
 221200-011-G02&t3=2000-12-22&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 283.  
 Location/Qualifiers  
 1..283  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="RT0055"  
 /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

Query Match 100.0%; Score 18; DB 2; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTCGGCTCTCGGCTGC 18  
 |||||  
 Db 158 CTTTCGGCTCTCGGCTGC 175

RESULT 6  
 AW820481/c  
 LOCUS  
 DEFINITION QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW820481  
 VERSION AW820481.1 GI:7913475  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 332)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

```

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=1&t2=QV2-ST0298-140
200-042-f12&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
FEATURES
    source
        Location/Qualifiers
            1..332
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="ST0298"
                /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
ORIGIN
    Query Match      100.0%; Score 18; DB 2; Length 332;
    Best Local Similarity 100.0%; Pred. No. 2.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTCGGCTCTCGGCTGC 18
    ||||||||||||||||
Db 216 CTTTCGGCTCTCGGCTGC 199

RESULT 7
BE925384/c
LOCUS
DEFINITION
PMO-AN0087-180800-001-b07 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BE925384.1 GI:10451460
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 339)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Seq primer: puc 18 forward
High quality sequence stop: 339.
FEATURES
    source
        Location/Qualifiers
            1..339
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="AN0087"
                /note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
ORIGIN
    Query Match      100.0%; Score 18; DB 2; Length 339;
    Best Local Similarity 100.0%; Pred. No. 2.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTCGGCTCTCGGCTGC 18
    ||||||||||||||||
Db 56 CTTTCGGCTCTCGGCTGC 39

RESULT 8
AW820530/c
LOCUS
DEFINITION
QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW820530
VERSION
AW820530.1 GI:7913524
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 358)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=1&t2=QV2-ST0298-220
200-061-d10&t3=2000-02-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 358.
FEATURES
    source
        Location/Qualifiers
            1..358
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="ST0298"
                /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application

```

No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 358;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 230 CTTTCGGCTCTCGGCTGC 213

## RESULT 9

BM818649/c

## LOCUS

DEFINITION K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03  
5', mRNA sequence.

## ACCESSION

BM818649

## VERSION

BM818649.1 GI:19175062

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 396)

## AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.

## TITLE

21C Frontier Korean EST Project 2001

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Kim YS

## FEATURES

1..396

Location/Qualifiers

source

1..396

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S20T665307-4-F03"

/sex="M"

/lab\_host="Top10P"

/clone\_lib="S20T665307"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10P by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

## ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 249 CTTTCGGCTCTCGGCTGC 232

## RESULT 10

BI051278

## LOCUS

DEFINITION

ACCESSION

BI051278

VERSION

BI051278.1 GI:14458808

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 418)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PUBMED

10737800

COMMENT

Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-  
110101-607-f03&t3=2001-01-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 3

High quality sequence stop: 418.

Location/Qualifiers

source

1..418

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1:  
SmaI; Site 2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (O.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

## ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy 1 CTTTCGGCTCTCGGCTGC 18

|||||

Db 110 CTTTCGGCTCTCGGCTGC 127

## RESULT 11

BM741875/c

## LOCUS

DEFINITION

BM741875

K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-C01 5',  
mRNA sequence.

Query Match 100.0%; Score 18; DB 4; Length 396;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0;

```

ACCESSION   BM741875
VERSION     BM741875.1  GI:19063204
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 418)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            High quality sequence stop: 418.
            Location/Qualifiers
                1..418
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="S6SNU620-4-C01"
                /sex="F"
                /tissue_type="Aescites"
                /cell_type="Scattering floating"
                /cell_line="SNU-620"
                /lab_host="Top10F"
                /clone_lib="S6SNU620"
                /notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
                Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."

FEATURES             source
    source
    1..442
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1518718"
    /tissue_type="pooled germ cell tumors"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP GC4"
    /note="Vector: p7T73D-Pac (Pharmacia) with a modified
    polylinker; 1st strand cDNA was prepared from 3 pooled
    germ cell tumors, and was then primed with a Not I -
    oligo(dt) primer. Double-stranded cDNA was ligated to Eco
    RI adaptors (Pharmacia), digested with Not I and cloned
    into the Not I and Eco RI sites of the modified p7T73
    vector. Library is normalized. Library was constructed by
    Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 354 CTTTCGGCTCTCGGCTGC 371
    |||||

RESULT 13
BM818387/c
LOCUS
DEFINITION      K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
                5', mRNA sequence.
ACCESSION       BM818387
VERSION         BM818387.1  GI:19174800
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 447)
AUTHORS         Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                Kim,Y.S.
TITLE           21C Frontier Korean EST Project 2001
JOURNAL         Unpublished (2002)
COMMENT         Contact: Kim YS
                Genome Research Center
                Korea Research Institute of Bioscience & Biotechnology
                52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                Tel: +82-42-860-4470
                Fax: +82-42-860-4409
                Email: yongsung@mail.kribb.re.kr
                Plate: 3 row: B column: 02
                High quality sequence stop: 447.

QY 1 CTTTCGGCTCTCGGCTGC 18
    |||||
Db 121 CTTTCGGCTCTCGGCTGC 104
    |||||

RESULT 12
AA903741
LOCUS
DEFINITION      ok64a12.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518718 3,
                similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;, mRNA
                sequence.
ACCESSION       AA903741
VERSION         AA903741.1  GI:3038864
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



```

FEATURES
  source
    Location/Qualifiers
    1. .447
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="S20T665307-3-B02"
      /sex="M"
      /lab_host="Top10P"
      /clone_lib="S20T665307"
      /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
  Query Match 100.0%; Score 18; DB 4; Length 447;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18
   |||||
Db 249 CTTTCGGCTCTCGGCTGC 232

RESULT 14
BE378810/c
LOCUS
DEFINITION 601237325P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609126 5',
mRNA sequence.
ACCESSION BE378810
VERSION BE378810.1 GI:9324175
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 482)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Ling Hong/Rubin Laboratory
  DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLCM263 row: b column: 07
  High quality sequence start: 4
  High quality sequence stop: 479.
  High quality sequence stop: 479.
  Location/Qualifiers
  1. .482
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3609126"
    /tissue_type="endometrium, adenocarcinoma cell line"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_44"

```

```

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life technologies)."
```

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 482;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCGGCTCTCGGCTGC 18  
 |||||  
 Db 187 CTTTCGGCTCTCGGCTGC 170

RESULT 15  
 BM857244/c  
 LOCUS  
 DEFINITION K-EST0141477 S21SNU520 Homo sapiens cDNA clone S21SNU520-78-F09 5',  
 mRNA sequence.  
 ACCESSION BM857244  
 VERSION BM857244.1 GI:19213643  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 503)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 78 row: F column: 09  
 High quality sequence stop: 503.  
 High quality sequence stop: 503.

FEATURES  
 source  
 1. .503  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S21SNU520-78-F09"  
 /sex="F"  
 /tissue\_type="Stomach"  
 /cell\_type="Floating aggregates"  
 /cell\_line="SNU-520"  
 /lab\_host="Top10P"  
 /clone\_lib="S21SNU520"  
 /note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 503;  
Best/Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGGCTCTCGGCTGC 18  
|||||  
Db 429 CTTTCGGCTCTCGGCTGC 412

Search completed: February 5, 2005, 08:11:53  
Job time : 2147.2 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 18:10:39 ; Search time 432.664 Seconds  
(without alignments)  
1967.381 Million cell updates/sec

Title: US-09-753-169A-13  
Perfect score: 18  
Sequence: 1 aaccagcggtgaagcgt 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_pa.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	BD235161
2	18	100.0	18	6	BD235182
3	18	100.0	18	6	BD235183
4	18	100.0	18	6	AR140001
5	18	100.0	127	6	CQ112670
6	18	100.0	127	6	CQ151543
7	18	100.0	127	6	CQ185285
8	18	100.0	127	6	CQ234920
9	18	100.0	127	6	CQ272476
10	18	100.0	127	6	CQ310145
11	18	100.0	127	6	CQ346752
12	18	100.0	387	6	CQ732731
13	18	100.0	587	6	CQ099589
14	18	100.0	587	6	CQ138575
15	18	100.0	587	6	CQ175406
16	18	100.0	587	6	CQ221990
17	18	100.0	587	6	CQ259935
18	18	100.0	587	6	CQ297711
19	18	100.0	587	6	CQ334058

c 20	18	100.0	636	6	BD097037
c 21	18	100.0	702	6	BD084108
c 22	18	100.0	702	6	BD102202
c 23	18	100.0	702	9	BT007208
c 24	18	100.0	702	12	BT008248
c 25	18	100.0	737	6	AR054022
c 26	18	100.0	737	6	AR172595
c 27	18	100.0	737	6	IS2012
c 28	18	100.0	737	6	AR371662
c 29	18	100.0	737	6	AR380913
c 30	18	100.0	737	9	HSBCLXS
c 31	18	100.0	926	6	AR054021
c 32	18	100.0	926	6	AR118504
c 33	18	100.0	926	6	AR124952
c 34	18	100.0	926	6	AR144311
c 35	18	100.0	926	6	AR172594
c 36	18	100.0	926	6	BD243042
c 37	18	100.0	926	6	CQ765842
c 38	18	100.0	926	6	E58777
c 39	18	100.0	926	6	IS2011
c 40	18	100.0	926	6	AR371661
c 41	18	100.0	926	6	AR380885
c 42	18	100.0	926	6	AX839772
c 43	18	100.0	926	6	AX925686
c 44	18	100.0	926	9	HSBCLXL
c 45	18	100.0	1236	6	AX085490

## ALIGNMENTS

RESULT 1  
BD235161  
LOCUS BD235161 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xl.  
ACCESSION BD235161  
VERSION BD235161.1 GI:33044931  
KEYWORDS JP 2002519048-A/13.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xl  
JOURNAL Patent: JP 2002519048-A 13 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/13  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC A61K47/42,  
PC A61K47/48, A61K48/00, A61P35/00, C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACCAGCGTGAAGCGT 18  
|||||

Db 1 AACACGCGTTGAAGCGT 18

RESULT 2  
LOCUS BD235182 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide inhibitors of bcl-xL.  
VERSION BD235182.1 GI:33044952  
KEYWORDS JP 2002519048-A/34.  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Stein, C.A.  
TITLE Oligonucleotide inhibitors of bcl-xL  
JOURNAL Patent: JP 2002519048-A 34 02-JUL-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Artificial Sequence  
PN JP 2002519048-A/34  
PD 02-JUL-2002  
PF 02-JUL-1999 JP 2000557839  
PR 02-JUL-1998 US 09/109614  
PI CY A STEIN  
PC

C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC  
A61K47/42,  
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00  
CC ANTISENSE OLIGONUCLEOTIDE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
CC PHOSPHOROTHIOATE LINKAGE  
FH Key Location/Qualifiers  
FT misc binding (1)..(4)  
FT misc binding (10)..(12)  
FT misc binding (15)..(18).  
FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18  
|||||  
Db 1 AACACGCGTTGAAGCGT 18  
|||||

RESULT 4  
LOCUS AR140001 87 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 1 from patent US 6207424.  
ACCESSION AR140001  
VERSION AR140001.1 GI:14482497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 87)  
AUTHORS Chou, Q., Maa, J. and Chang, C.  
TITLE Self-primed amplification system  
JOURNAL Patent: US 6207424-A 1 27-MAR-2001;  
FEATURES  
source  
Location/Qualifiers  
1..87  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 87;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18  
|||||  
Db 70 AACACGCGTTGAAGCGT 87  
|||||

RESULT 5  
LOCUS CQ112670 127 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 21529 from Patent WO0157272.  
ACCESSION CQ112670  
VERSION CQ112670.1 GI:41082540  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 21529 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncfe="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACACGCGGTTGAAGCGT 18
|||||
Db 51 AACACGCGGTTGAAGCGT 68
RESULT 6
CQ151543
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 21565 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncfe="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 5.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACACGCGGTTGAAGCGT 18
|||||
Db 51 AACACGCGGTTGAAGCGT 68
RESULT 7
CQ185285
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in adult liver, signal
Patent: WO 0157273-A 21759 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncfe="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACACGCGGTTGAAGCGT 18
|||||
Db 51 AACACGCGGTTGAAGCGT 68
RESULT 8
CQ234920
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 21759 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncfe="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACACGCGGTTGAAGCGT 18
|||||
Db 51 AACACGCGGTTGAAGCGT 68
RESULT 9
CQ185285
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 21529 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .127
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncfe="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACACGCGGTTGAAGCGT 18
|||||
Db 51 AACACGCGGTTGAAGCGT 68
```

```

CQ272476
LOCUS       CQ272476               127 bp    DNA             linear      PAT 23-JAN-2004
DEFINITION   Sequence 20737 from Patent WO0157277.
ACCESSION    CQ272476
VERSION      CQ272476.1   GI:41245080
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 20737 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
              HIT: AWB20481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 51 AACACGCGTTGAAGCGT 68

RESULT 10
CQ310145
LOCUS       CQ310145               127 bp    DNA             linear      PAT 23-JAN-2004
DEFINITION   Sequence 21250 from Patent WO0186003.
ACCESSION    CQ310145
VERSION      CQ310145.1   GI:41270722
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
              2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AWB20481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 51 AACACGCGTTGAAGCGT 68

CQ272476
LOCUS       CQ272476               127 bp    DNA             linear      PAT 23-JAN-2004
DEFINITION   Sequence 20737 from Patent WO0157277.
ACCESSION    CQ272476
VERSION      CQ272476.1   GI:41245080
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human fetal liver
JOURNAL      Patent: WO 0157277-A 20737 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
              = 4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
              HIT: AWB20481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 51 AACACGCGTTGAAGCGT 68

CQ310145
LOCUS       CQ310145               127 bp    DNA             linear      PAT 23-JAN-2004
DEFINITION   Sequence 21250 from Patent WO0186003.
ACCESSION    CQ310145
VERSION      CQ310145.1   GI:41270722
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human lung
JOURNAL      Patent: WO 0186003-A 21250 15-NOV-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
              2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AWB20481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 51 AACACGCGTTGAAGCGT 68

CQ346752
LOCUS       CQ346752               127 bp    DNA             linear      PAT 23-JAN-2004
DEFINITION   Sequence 20846 from Patent WO0157275.
ACCESSION    CQ346752
VERSION      CQ346752.1   GI:41295823
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human brain
JOURNAL      Patent: WO 0157275-A 20846 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..127
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL =
              2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
              AWB20481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
              1.00e-65"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 51 AACACGCGTTGAAGCGT 68

CQ732731
LOCUS       CQ732731               387 bp    DNA             linear      PAT 03-FEB-2004
DEFINITION   Sequence 18665 from Patent WO02068579.
ACCESSION    CQ732731
VERSION      CQ732731.1   GI:42313858
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
              humanexons or transcripts, for detecting expression and other uses
              thereof
JOURNAL      Patent: WO 02068579-A 18665 06-SEP-2002;
              PE Corporation (NY) (US)
FEATURES     Location/Qualifiers
              source
                1..387
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18
    |||||
Db 326 AACACGCGTTGAAGCGT 309

RESULT 13
CQ099589

```

```
LOCUS      CQ099589          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 8448 from Patent WO0157272.
ACCESSION  CQ099589
VERSION    CQ099589.1  GI:41068615
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human placenta
JOURNAL   Patent: WO 0157272-A 8448 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES   source
            Location/Qualifiers
            1..587
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL =
            1.5"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTTGAAGCGT 18
        |||||
Db      450 AACACGCGGTTGAAGCGT 467

RESULT 14
LOCUS      CQ138575          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 8597 from Patent WO0157276.
ACCESSION  CQ138575
VERSION    CQ138575.1  GI:41095941
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
JOURNAL   Patent: WO 0157276-A 8597 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES   source
            Location/Qualifiers
            1..587
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
            = 5.5"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTTGAAGCGT 18
        |||||
Db      450 AACACGCGGTTGAAGCGT 467

RESULT 15
LOCUS      CQ175406          587 bp      DNA      linear      PAT 21-JAN-2004
DEFINITION Sequence 6802 from Patent WO0157274.
ACCESSION  CQ175406
```

```
VERSION    CQ175406.1  GI:41170145
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human heart
JOURNAL   Patent: WO 0157274-A 6802 09-AUG-2001;
            Aecomica, Inc. (US)
FEATURES   source
            Location/Qualifiers
            1..587
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL117381.9-EXPRESSED IN HEART, SIGNAL = 1.6"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 587;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACACGCGGTTGAAGCGT 18
        |||||
Db      450 AACACGCGGTTGAAGCGT 467

Search completed: February 4, 2005, 23:30:42
Job time : 432.664 secs
```

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 15:50:53 ; Search time 232.23 Seconds  
(without alignments)  
406.880 Million cell updates/sec

Title: US-09-753-169A-13  
Perfect score: 18  
Sequence: 1 aaccagcggttgagcgt 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1:	Geneseqn1980s:*
2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	3	AZ46983 Bcl-Xl MR
2	18	100.0	87	4	Aah19915 Single SN
3	18	100.0	127	4	Aba72432 Human foe
4	18	100.0	127	4	Aai52843 Probe #21
5	18	100.0	127	4	Aba38215 Probe #16
6	18	100.0	127	4	Aak47008 Human bon
7	18	100.0	127	4	Aak20855 Human bra
8	18	100.0	127	4	Abs46769 Human liv
9	18	100.0	127	6	ABs21259 Human gen
10	18	100.0	179	12	ACH84269 Human gen
11	18	100.0	299	10	ACD94503 Human col
12	18	100.0	337	10	ADK66037 Standardi
13	18	100.0	492	9	ACH46093 Human inf
14	18	100.0	587	4	ABA59891 Human foe
15	18	100.0	587	4	RAI139762 Probe #84
16	18	100.0	587	4	ABA28336 Probe #68
17	18	100.0	587	4	AAK34040 Human bon
18	18	100.0	587	4	AAK08161 Human bra
19	18	100.0	587	4	ABS33839 Human liv
20	18	100.0	587	6	ABS08825 Human gen
21	18	100.0	587	12	ACH70569 Human gen

c	22	18	100.0	636	4	AAH48169	Aah48169 Mutant bc
c	23	18	100.0	702	5	AAH43464	Aah43464 cDNA clon
c	24	18	100.0	702	12	ADM45994	Adm45994 Human apo
c	25	18	100.0	737	2	AAQ81699	Aaq81699 Human thy
c	26	18	100.0	737	10	ABZ83507	Abz83507 Toxicolog
c	27	18	100.0	737	11	ADI32132	Adi32132 Human cdn
c	28	18	100.0	926	2	AAQ81698	Aaq81698 Human thy
c	29	18	100.0	926	2	AAT40079	Aat40079 Bcl-XL ge
c	30	18	100.0	926	3	AAZ93614	Aaz93614 Bcl-x gen
c	31	18	100.0	926	4	AAZ93614	Aaz93614 Bcl-x gen
c	32	18	100.0	926	4	AAC90810	Aac90810 Human bcl
c	33	18	100.0	926	6	ABK84766	Abk84766 Human cdn
c	34	18	100.0	926	8	ABT16641	Abt16641 Human bcl
c	35	18	100.0	926	10	ADD56779	Add56779 Human bcl
c	36	18	100.0	926	10	AAD64187	Aad64187 Human bcl
c	37	18	100.0	926	11	ADI32104	Adi32104 Human cdn
c	38	18	100.0	926	12	ADH52630	Adh52630 Human ant
c	39	18	100.0	926	12	ADO19990	Ado19990 Human pro
c	40	18	100.0	926	12	ADP13351	Adp13351 Renal cel
c	41	18	100.0	1236	5	AAS00247	Aas00247 Bcl-XI-DT
c	42	18	100.0	2386	10	ADG89403	Adg89403 Cancer de
c	43	18	100.0	2386	12	ADN04260	Adn04260 Antipsori
c	44	18	100.0	2575	12	ADO19866	Ado19866 Human pro
c	45	18	100.0	7372	2	AAx33182	Aax33182 Base sequ

ALIGNMENTS

RESULT 1  
AAZ46983  
ID AAZ46983 standard; DNA; 18 BP.  
XX  
AC AAZ46983;  
XX  
DT 14-APR-2000 (first entry)  
XX  
DE Bcl-Xl mRNA specific antisense oligo M.  
XX  
KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
XX lung; bladder; bcl-2; vascular lesion; antisense; ss.  
OS Homo sapiens.  
XX  
PN WC200001393-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 02-JUL-1999; 99WO-US015250.  
XX  
PR 02-JUL-1998; 98US-00109614.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
Stein CA;  
XX  
WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.  
Claim 1; Fig 1; 69pp; English.  
The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso- (4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-XL mRNA

XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18  
 |||||  
 Db 1 AACACGCGGTTGAAGCGT 18

RESULT 2  
 AAH19915  
 ID AAH19915 standard; DNA; 87 BP.  
 AC AAH19915;  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE Single SNAP primer SPAS-BCL-1001 directed toward bcl-xS and bcl-xL.  
 XX  
 KW Self-priming nucleic acid polymerase; SNAP; primer; amplification; BCL;  
 KW bcl-xS; bcl-xL; human; ss.  
 OS Homo sapiens.  
 XX  
 PN US6207424-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 23-NOV-1999; 99US-00447942.  
 XX  
 PR 23-NOV-1999; 99US-00447942.  
 XX

PA (MAXI-) MAXIM BIOTECH INC.  
 XX  
 PI Chou Q, Maa J, Chang C;  
 XX  
 DR WPI; 2001-298942/31.  
 XX  
 PT New self-priming nucleic acid polymerase primer for copying target  
 PT nucleic acid, contains (anti) sense target specific and non-target  
 PT (anti)sense primer binding domains.  
 XX  
 PS Claim 45; Col 18; 20pp; English.  
 CC  
 CC The present invention describes a self-priming nucleic acid polymerase  
 CC (SNAP) primer (I) for copying a target nucleic acid (TNA) comprising,  
 CC from 3'-5', a sense, target-specific binding domain (TBD), a non-target,  
 CC antisense primer binding domain (PBD), non-target, sense PBD and an  
 CC antisense TBD. SNAP primers are useful for copying a target nucleic acid  
 CC or a mixture of at least two different target nucleic acids. Methods  
 CC comprising SNAPS are less likely to produce variable and erroneous  
 CC signals in multiplex assays. The present sequence represents a  
 CC specifically claimed single SNAP primer designated SPAS-BCL-1001, which  
 CC is directed toward bcl-xS and bcl-xL

XX  
 XX Sequence 87 BP; 19 A; 26 C; 24 G; 18 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 4; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18  
 |||||  
 Db 70 AACACGCGGTTGAAGCGT 87

RESULT 3  
 ABA72432  
 ID ABA72432 standard; DNA; 127 BP.  
 XX  
 AC ABA72432;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human foetal liver single exon nucleic acid probe #20737.  
 XX  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human fetal liver.  
 XX  
 PS Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.  
 XX

CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 4; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGGTTGAAGCGT 18  
 |||||  
 Db 51 AACACGCGGTTGAAGCGT 68

RESULT 4  
 AAI52843  
 ID AAI52843 standard; DNA; 127 BP.  
 XX  
 AC AAI52843;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Probe #21529 used to measure gene expression in human placenta sample.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 XX  
 OS Homo sapiens.

```
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX Claim 25; SEQ ID NO 21529; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 127.BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. NO. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AACACGCGGTTGAAGCGT 18
Db 51 AACACGCGGTTGAAGCGT 68
XX
RESULT 5
ABA38215
ID ABA38215 standard; DNA; 127 BP.
XX
XX ABA38215;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #16681 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX WO200157274-A2.
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
XX
Query Match 100.0%; Score 18; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. NO. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AACACGCGGTTGAAGCGT 18
Db 51 AACACGCGGTTGAAGCGT 68
XX
RESULT 6
AAK47008
ID AAK47008 standard; DNA; 127 BP.
XX
XX AAK47008;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 21565.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
XX WO200157276-A2.
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
XX
```

XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention  
XX  
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AACACGCGTTGAAGCGT 18  
DB 51 AACACGCGTTGAAGCGT 68  
|||||  
RESULT 7  
AAK20855  
ID AAK20855 standard; DNA; 127 BP.  
AC AAK20855;  
XX  
XX  
XX 05-NOV-2001 (first entry)  
XX Human brain expressed single exon probe SEQ ID NO: 20846.  
DE Human; brain expressed exon; gene expression analysis; probe; microarray;  
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KW ss.  
KW  
XX Homo sapiens.  
OS  
XX WO200157275-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000667.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
XX brains.  
XX  
XX Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English.  
PS  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention  
XX  
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18  
DB 51 AACACGCGTTGAAGCGT 68  
|||||  
RESULT 8  
ABS46769  
ID ABS46769 standard; DNA; 127 BP.  
XX  
XX  
XX ABS46769;  
XX  
XX 25-FEB-2003 (first entry)  
XX  
XX Human liver single exon probe, SEQ ID NO 21759.  
DE  
XX Human; single exon nucleic acid probe; liver; cirrhosis;  
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; ss.  
KW  
XX Homo sapiens.  
OS  
XX WO200157273-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488898/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human adult liver.  
XX  
XX Claim 4; SEQ ID NO 21759; 658pp; English.  
XX  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
XX measuring human gene expression in a sample derived from human adult  
XX liver, comprising one of 13109 defined nucleotide sequences given in the  
XX specification (or complements/ fragments). The probe hybridises at high  
XX stringency to a nucleic acid molecule expressed in the human adult liver.  
XX (I) may be used for predicting, measuring and displaying gene expression  
XX in samples derived from human adult liver. The genes identified may be  
XX involved in genetic liver diseases such as cirrhosis,  
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
XX associated with coronary heart disease. ABS25011-ABS51005 represent human  
XX liver single exon nucleic acid probes of the invention. Note: The  
XX sequence information for this patent does not appear in the printed  
XX specification but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;  
SQ  
  
Query Match 100.0%; Score 18; DB 4; Length 127;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18  
DB 51 AACACGCGTTGAAGCGT 68  
|||||

RESULT 9  
ABS21259  
ID ABS21259 standard; DNA; 127 BP.  
XX  
AC ABS21259;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 21250.  
XX  
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease; open reading frame; ORF.  
XX  
OS Homo sapiens.  
XX  
PN WO200186003-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000665.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2002-114183/15.  
XX  
PT Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples.  
XX  
PS Claim 4; SEQ ID NO 21250; 634pp; English.  
XX  
CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of probes  
CC; the novel set of probes which hybridize at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 AACCCAGCGGTTGAAGCGT 18  
Db 51 AACCCAGCGGTTGAAGCGT 68  
RESULT 10  
ACH84269/c  
ID ACH84269 standard; DNA; 179 BP.  
XX  
AC ACH84269;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon probe #17464.  
XX  
KW Human; probe; ss; gene expression; single exon probe; microarray;  
KW alternative splicing event; genomic alteration.  
XX  
OS Homo sapiens.  
XX  
PN US2003194704-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 03-APR-2002; 2002US-00029386.  
XX  
PR 03-APR-2002; 2002US-00029386.  
XX  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
XX  
PI Penn SG, Rank DR, Hanzel DK;  
XX  
DR WPI; 2004-119264/12.  
XX  
PT New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
PS Claim 1; SEQ ID NO 17464; 80pp; English.  
XX  
CC The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and  
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
CC fully defined in the specification. The probe is a single exon probe that  
CC hybridises under high stringency conditions to a nucleic acid molecule  
CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single



PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.  
XX Koehler T, Rost A;  
XX WPI; 2003-732912/70.  
DR Standardized polynucleotide system, useful for quantitative, real-time  
XX determination of nucleic acid, comprises stabilized standards, primers  
PT and probe.  
XX  
XX Claim 1; Page 7; 38pp; German.  
XX  
XX The present invention relates to a standardized polynucleotide system,  
CC which comprises at least one carrier nucleic acid, at least 3  
CC oligonucleotides, as primers and target-specific, fluorescently labeled  
CC probe and optionally at least one set of stabilized controls (standard  
CC RNA or DNA) of known concentration and instructions. The system comprises  
CC any of 20 sets of one control, two primers and one target-specific probe.  
CC The standardized polynucleotide system can be used for quantitative, real  
CC time detection of target nucleic acids, especially analysis of genes or  
CC gene products, e.g. for individualized medical diagnosis, in veterinary  
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,  
CC pharmaceutical testing, analysis of food or environmental samples and  
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present  
CC sequence is a polynucleotide used in the system of the invention.  
XX  
XX Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 18; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACACGCGGTGAAGCGT 18  
DB 238 AACACGCGGTGAAGCGT 221  
RESULT 13  
ACH46093/c  
ID ACH46093 standard; cDNA; 492 BP.  
XX  
AC ACH46093;  
XX  
DT 13-OCT-2003 (first entry)  
DE Human infant brain cDNA #156.  
XX  
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN US2003073623-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 30-JUL-2001; 2001US-00918995.  
XX  
PR 30-JUL-2001; 2001US-00918995.  
XX  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
XX  
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX  
XX WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating

PT antisense DNA or RNA.  
XX  
PS Claim 1; SEQ ID NO 33305; 4pp; English.  
XX  
XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations,  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
XX  
SQ Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 9; Length 492;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACACGCGGTGAAGCGT 18  
DB 422 AACACGCGGTGAAGCGT 405  
RESULT 14  
ABA59891  
ID ABA59891 standard; DNA; 587 BP.  
XX  
AC ABA59891;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human foetal liver single exon nucleic acid probe #8196.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US0000669.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human fetal liver.  
PS Claim 1; SEQ ID NO 8196; 639pp + Sequence Listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring  
CC

CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18  
|||  
Db 450 AACACGCGTTGAAGCGT 467

## RESULT 15

AAI39762  
ID AAI39762 standard; DNA; 587 BP.

XX  
AC AAI39762;

DT 17-OCT-2001 (first entry)

DE Probe #8448 used to measure gene expression in human placenta sample.

KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder; ss.

XX Homo sapiens.

PN WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000663.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 8448; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders

XX Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 587;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGTTGAAGCGT 18  
|||  
Db 450 AACACGCGTTGAAGCGT 467

Db 450 AACACGCGTTGAAGCGT 467

Search completed: February 4, 2005, 21:52:44  
Job time : 232.23 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 20:41:45 ; Search time 2146.2 Seconds  
(without alignments)  
305.616 Million cell updates/sec

Title: US-09-753-169A-13

Perfect score: 18

Sequence: 1 aaccagcggttgagcgt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsl1:\*

9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	140	2	BF948716 CM2-NN115
2	18	100.0	154	2	AW849455 IL3-CT021
3	18	100.0	167	2	BF929309 IL2-NT020
4	18	100.0	194	2	BF880488 QV3-ET017
5	18	100.0	216	2	BF806802 PM2-CI011
6	18	100.0	232	2	BF804861 PM2-CI011
7	18	100.0	233	1	AI904167 CM-BT043
8	18	100.0	283	2	BF823588 RC5-RT005
9	18	100.0	332	2	AW820481 QV2-ST029
10	18	100.0	339	2	BE925384 PM0-AN008
11	18	100.0	358	2	AW820530 QV2-ST029
12	18	100.0	396	4	BM818649 K-EST0085
13	18	100.0	418	4	BI051278 CM3-GN029
14	18	100.0	418	4	BM741875 K-EST0014
15	18	100.0	437	7	W01420 za73d06.xl
16	18	100.0	442	1	AA903741 ok64a12.s
17	18	100.0	447	1	BM818387 K-EST0085
18	18	100.0	482	2	BE378810 601237325
19	18	100.0	486	2	AW814883 MR1-ST020
20	18	100.0	503	4	BM857244 K-EST0141
21	18	100.0	516	7	H09884 ym05b07.xl
22	18	100.0	522	2	BE395937 601312716
23	18	100.0	528	6	CB118773 K-EST0165
24	18	100.0	555	2	BE393580 601310279

25	18	100.0	559	1	AI133331
26	18	100.0	563	2	BE617040
27	18	100.0	579	4	BM741157 K-EST0013
28	18	100.0	607	5	B0636684 hdl3a09.y
29	18	100.0	620	4	BM820164 K-EST0088
30	18	100.0	652	4	BM043798 603620649
31	18	100.0	681	6	CF147016 UI-HF-C80
32	18	100.0	687	2	BE293685 601186941
33	18	100.0	695	4	BI252492 602952957
34	18	100.0	697	4	BI457116 603185360
35	18	100.0	699	2	BE870269 601447403
36	18	100.0	700	4	BE8831301 602766132
37	18	100.0	705	4	BE290422 602388270
38	18	100.0	714	4	BG470667 602511594
39	18	100.0	720	6	CD636470 56049223J
40	18	100.0	725	6	CD636468 56049107J
41	18	100.0	728	4	BG169629 602312189
42	18	100.0	737	4	BG748447 602706419
43	18	100.0	739	4	BG437506 602489238
44	18	100.0	765	2	BF569393 602185659
45	18	100.0	765	2	BE873153 601451667

#### ALIGNMENTS

RESULT 1  
BF948716  
LOCUS BF948716 140 bp mRNA linear EST 22-JAN-2001  
DEFINITION CM2-NN1152-311000-454-b02 NN1152 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BF948716  
VERSION BF948716.1 GI:12365991  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 140)  
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 31  
High quality sequence stop: 140.

#### FEATURES

source  
1. 140  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NN1152"

/note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACACGCGTTGAAGCGT 18

Db 104 AACACGCGTTGAAGCGT 121

## RESULT 2

AW849455

## LOCUS

DEFINITION AW849455 154 bp mRNA linear EST 19-MAY-2000  
IL3-CT0215-170300-093-F10\_1 CT0215 Homo sapiens cDNA, mRNA  
sequence.

## ACCESSION

VERSION AW849455

## KEYWORDS

SOURCE EST.

## ORGANISM

Homo sapiens (human)

## REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

## TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=IL3-CT0215-170300-093-F10.1&t3=2000-03-17&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 52.

## FEATURES

source

1. .154

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CT0215"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1 AACACGCGTTGAAGCGT 18

Db 121 AACACGCGTTGAAGCGT 138

## RESULT 3

BF929309

## LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 167)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL2-NT0202-081200-298-D05&t3=2000-12-08&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 167.

FEATURES

source

1. .167

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="NT0202"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match

Best Local Similarity

Matches 18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1 AACACGCGTTGAAGCGT 18

Db 87 AACACGCGTTGAAGCGT 104

## RESULT 4

BF880488

## LOCUS

DEFINITION

ACCESSION

BF880488

QV3-ET0175-011200-514-a04 ET0175 Homo sapiens cDNA, mRNA sequence.

Query Match

Best Local Similarity

Matches 18; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

```

VERSION      BF80488.1  GI:12270718
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 194)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-
             011200-514-a04&t3=2000-12-01&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 17
             High quality sequence stop: 194.
             Location/Qualifiers
FEATURES     source
             1..194
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="ET0175"
             /note="Organ: lung tumor; Vector: puc18; Site:1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORFEST PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACCCAGCGGTGAAGCGT 18
       |||||
Db      146 AACCCAGCGGTGAAGCGT 163

RESULT 5
BF806802
LOCUS      PM2-CI0111-091100-004-B10 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION  BF806802
VERSION     BF806802.1  GI:12135791
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 216)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-
             011200-514-a04&t3=2000-12-01&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 17
             High quality sequence stop: 194.
             Location/Qualifiers
FEATURES     source
             1..216
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="CI0111"
             /note="Organ: colon ins; Vector: puc18; Site:1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORFEST PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACCCAGCGGTGAAGCGT 18
       |||||
Db      86  AACCCAGCGGTGAAGCGT 103

RESULT 6
BF804861
LOCUS      PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION  BF804861
VERSION     BF804861.1  GI:12133850
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 232)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-
             091100-004-B10&t3=2000-11-09&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 25
             High quality sequence stop: 216.
             Location/Qualifiers
FEATURES     source
             1..216
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="CI0111"
             /note="Organ: colon ins; Vector: puc18; Site:1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORFEST PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACCCAGCGGTGAAGCGT 18
       |||||
Db      86  AACCCAGCGGTGAAGCGT 103

```

```

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-
             091100-004-B10&t3=2000-11-09&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 25
             High quality sequence stop: 216.
             Location/Qualifiers
FEATURES     source
             1..216
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="CI0111"
             /note="Organ: colon ins; Vector: puc18; Site:1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORFEST PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACCCAGCGGTGAAGCGT 18
       |||||
Db      86  AACCCAGCGGTGAAGCGT 103

RESULT 6
BF804861
LOCUS      PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION  BF804861
VERSION     BF804861.1  GI:12133850
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 232)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-
             091100-004-B10&t3=2000-11-09&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 25
             High quality sequence stop: 216.
             Location/Qualifiers
FEATURES     source
             1..216
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /dev_stage="Adult"
             /clone_lib="CI0111"
             /note="Organ: colon ins; Vector: puc18; Site:1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORFEST PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACCCAGCGGTGAAGCGT 18
       |||||
Db      86  AACCCAGCGGTGAAGCGT 103

```

Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml.pl?ti=PM2&t2=PM2-CI0111-041100-001-d01&t3=2000-11-04&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 13  
 High quality sequence stop: 232.

## FEATURES

source

1. .232  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="CI0111"  
 /note="Organ: colon\_ins; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTGAAGCGT 18  
 |||||  
 Db 102 AACACGCGGTGAAGCGT 119

## RESULT 7

AI904167/c  
 LOCUS AI904167 233 bp mRNA linear EST 30-MAR-2000  
 DEFINITION CW-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AI904167  
 VERSION AI904167.1 GI:6494554  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

AUTHORS  
 1 (bases 1 to 233)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/seq/gethtml.pl?ti=CM&t2=CM-BT043-089.html&t3=090299&t4=1>)

Seq primer: puc 18 forward.  
 Location/Qualifiers  
 1. .233  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /sex="female"  
 /dev\_stage="Adult"  
 /clone\_lib="BT043"  
 /note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the pUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTGAAGCGT 18  
 |||||  
 Db 75 AACACGCGGTGAAGCGT 58

## RESULT 8

BF823588  
 LOCUS BF823588 283 bp mRNA linear EST 13-JAN-2001  
 DEFINITION RC5-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF823588  
 VERSION BF823588.1 GI:12164528  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

AUTHORS  
 1 (bases 1 to 283)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC5&t2=RC5-RT0055-221200-011-G02&t3=2000-12-22&t4=1>)

Seq primer: puc 18 forward  
 High quality sequence stop: 283.

## FEATURES

source

1. .283  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="RT0055"  
 /note="Organ: kidney tumor; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products



```

VERSION      AW820530.1  GI:7913524
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE    1 (bases 1 to 358)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV2-ST0298-220
              200-061-d10&t3=2000-02-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 44
              High quality sequence stop: 358.

FEATURES     source
              1..358
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="ST0298"
                /dev_stage="Adult"
                /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the puc 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."

ORIGIN
Query Match      100.0%; Score 18; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
    |||||
Db 256 AACACGCGGTTGAAGCGT 239

RESULT 12
BM818649/c
LOCUS          BM818649          396 bp      mRNA      linear      EST 06-MAR-2002
DEFINITION    K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
              5', mRNA sequence.
ACCESSION     BM818649
VERSION       BM818649.1  GI:19175062
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 396)
AUTHORS      Kim,M.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
              Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 03
High quality sequence stop: 396.
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="S20T665307-4-F03"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then dephapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 18; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACACGCGGTTGAAGCGT 18
    |||||
Db 275 AACACGCGGTTGAAGCGT 258

RESULT 13
BI051278
LOCUS          BI051278          418 bp      mRNA      linear      EST 15-JUN-2001
DEFINITION    CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BI051278
VERSION       BI051278.1  GI:14458808
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 418)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.

TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics

```

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-  
110101-607-f03&t3=2001-01-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 3  
High quality sequence stop: 418.

## FEATURES

source

1. .418

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="GN0297"

/note="Organ: placenta normal; Vector: puc18; Site 1:  
SmaI; Site 2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCCAGCGTTGAAGCGT 18

|||||  
Db 84 AACCCAGCGTTGAAGCGT 101

RESULT 14  
BM741875/c  
LOCUS  
DEFINITION K-EST0014589 S6SNU620 Homo sapiens cDNA clone S6SNU620-4-C01 5',  
mRNA sequence.

ACCESSION BM741875

VERSION BM741875.1 GI:19063204

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 418)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 4 row: C column: 01

High quality sequence stop: 418.

Location/Qualifiers

1. .418

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="S6SNU620-4-C01"

/sex="F"

/tissue\_type="Ascites"

## FEATURES

source

1. .437

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1243109"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:298187"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal\_lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

/cell\_type="Scattering floating"

/cell\_line="SNU-620"

/lab\_host="Top10F"

/clone\_lib="S6SNU620"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 418;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCCAGCGTTGAAGCGT 18

|||||  
Db 147 AACCCAGCGTTGAAGCGT 130

## RESULT 15

W01420/c

LOCUS

DEFINITION z473d06.r1 Soares fetal\_lung NbHL19W Homo sapiens cDNA clone

IMAGE:298187 5' similar to SW:BCIX\_HUMAN Q07817 APOPTOSIS REGULATOR

BCL-X.; mRNA sequence.

ACCESSION W01420

VERSION W01420.1 GI:1273428

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 437)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,S., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IWGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 383.

Location/Qualifiers

1. .437

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1243109"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:298187"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal\_lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCAATCTGAGTGGGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGAGCGTTGAAGCGT 18  
 ||||||||||||||||  
 Db 403 AACGAGCGTTGAAGCGT 386

Search completed: February 5, 2005, 08:11:53  
 Job time : 2146.2 secs